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Listing first 45 summaries
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SUMMARIES

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ALIGNMENTS

REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	ATT3A5/c	RESULT 1
<pre>1 (bases 1 to 84196) Bloecker,H., Mewes,H.W., Lemcke,K., Mayer,K.F.X., Quetler;F. and Salanoubat,M.</pre>	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; endicotyledons; core eudicots; Rosidae; eurosids II; Brasslcales; Brassicaceae; Arabidopsis.	Arabidopsis thaliana	Arabidopsis thaliana.		AL132979.2 GI:6782244	AL132979	Arabidopsis thaliana DNA chromosome 3, BAC clone T3A5.	ATT3A5 84196 bp DNA linear PLN 26-JAN-2000		

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	CDS	gene	exon	intron	exon	intron	•	exon	intron	exon						CDS	gene	LTR	misc_	ב			FEATURES source		COMMENT				JOURNAL	AUTHORS TITLE	JOURNAL REFERENCE
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intron exon intron	exon	exon	intron	intron	exon	intron	exon									CDS	gene	· exon								CDS	gene	exon	intron	exon	•
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GWDFIGSTIGYLKPYTATTLGDFMQQHYSKYGKIYRSNLFGBPTIVSADAGLARETLQ
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; Pred. No. 1.1e-153;
0; Mismatches 0;
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                                                                                                                                                                                             Murphy, G., I
Unpublished
Submitted (25-JUL-2002) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK

AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a crap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. _3 denotes a sequence derived from the 3'end of the transposon, _5 denotes a sequence derived from the 5'end of the
                                                                                                                                                                                                                                                                                                                  STS; STS, sequence tagged site Arabidopsis thaliana. Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                        AL844732
Arabidopsis thaliana
                                                                                                                                              Clarke, J.H.
Direct Submission
                                                                                                                                                                                                                                Clarke, J.H.,
                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                               Jones, J.D.G. and Bevan,
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STS SM_3.29533, sequence
                                                                                                                                                                                                                   and Bevan, M.
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On-line see
code: N1157
                                                                                                                                                                Center, Stanford University, 855 California Avenue, Palo / 94304, USA
On Apr 2, 1999 this sequence version replaced gi:4337172.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                             Direct Submission
Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology
Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                             104992 bp Plasmodium falciparum chromosome ***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                          Hyman, R.W., Fung, E.L., and Davis, R.W.
                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum 3D7
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Alveolata;
1 (bases 1 to 104992)
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                                                                                                                                                                                                                                                                                  Hyman, R.W., Qin, F., Fung, E.L.,
                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum
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                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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be
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 Location/Qualifiers
1. .104992
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37 c 28 g 56 t
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/variety="Landsberg erecta"
/db_xref="taxon:3702"
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                       58642: contig of 58642 bp in length
58842: gap of unknown length
91011: contig of 32169 bp in length
91211: gap of unknown length
91212: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BSRC GARNet, ATIS project stock requests: http://nasc.nott.ac.uk/ NASC
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Pred. No. 3.8e-16;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                      Qin,F.,
                                                                                                                                                                                                                                                                                  Conway, A.B. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                      Tamaki,T.,
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CTCGACCCTTAAAAATACGATTTTACAGCGTCACTAGTTGAGATTACTAGCATAAAGCATA 1064
                                                                             AAAACAATTGTCTGGGGACCATTTTGAATAAACTTTTCTCAAACATTACGGGACACTGGA 1004
                                                                                                            TTTGTTTCGTTTCTTAACTATATTATCGCGGATATATGATAACAATGATATATCAC 944
                                                                                                                                                                    ATGAATTATTTAAATAATTAAAACAATAATATATATAAATTAATTATATTTAGTAAAT 73165
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                                                                                                                                                                                                                                                                                 TGACCCATGGAGTATGTGAAATAATTATCAAAAGAGATAAGAGATGACAACCAAAAGGTTG
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0326 c 9564
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/db_xref="taxon:5833"
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                                                                                                                                     AATTTTTGAAAAATGTTATAATTTCTAACAATATTATTAAAATATGATGCCTATAATGTA 2000
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                                                                                                                                                                                                                                                                                                                                                                                        TGTAACATTA-----CAATATTTATATTAGATACTAGTATGTGATTATTCCAAAT 1645
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                                                                                TTTCCTATGTTCTTAAAATATTTTTTTTTATATTTAGTTATAAATACATTATGAACCAAT 2060
                                                                                                                                                                  TAATTTAATTAATAATATTATATAATATTTATATTATTTGTTTAATATTTAATTACTATT 7418:
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108 ATAATTAAATATTAAAATTCATTTAAAATATTTACA-AGTAATTAATTATCTTTACATTG 166
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On Aug 12, 2000 this sequence version replaced gi:8810447.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
1 (bases 1 to 169546)
Hyman,R.W., Fung,E.L., Qin,F., Rowley,D., Mao,J.,
Kurdi,O.B., Conway,A.B. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W. Direct Submission
Submitted (19-FBB-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum 3D7
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium fa
PROGRESS ***,
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                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                             /clone="PFYAC293"
/clone="3D7"
15381 c 15705
                                                                                                                                                                                                                          /organism="Plasmodium
/db_xref="taxon:5833"
/chromosome="12"
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23666: gap of unknown length
169546: contig of 145880 bp in
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Plasmodium falciparum.
Plasmodium falciparum
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosp
1 (bases 1 to 169546)
Hyman, R. W., Fung, E.L., Qin, F., Rowley, D.,
Kurdi, O.B., Conway, A.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                      HTG;
                                                                                                                                                                                      AC004157
AC004157.8 GI:9797712
                                                                                                                                                                                                                                                        AC004157
Plasmodium
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                                                                                             Apicomplexa; Haemosporida; Plasmodium.
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                                                   Mao, J.,
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3D7, ***
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94304, USA
On Aug 12, 2000 this sequence version replaced gi:8810447.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
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Size Submitted (19-FEB-1998) Stanford DNA Sequencing and Technology Submitted (19-FEB-1998) Stanford DNA Sequence (19-FEB-1998) Stanford DNA Sequen
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Hyman, R.W., Qin, F., Fung, E.L.,
                                                                      GAGTAGTGACCCATGGAGTATGTGAATAATTATCAAAGAGAATAAGAGATGACAAACCAAA
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                            TTATTACATTATTAATATATATTTTTTTATTTAAAAAAATATAATTAAATAAATTAATT
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/db_xref="taxon:5833"
/chromosome="12"
/clone="ppyAC293"
/clone="3D7"
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23666: gap of unknown length
169546: contig of 145880 bp in
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Pred. No. 3.4e-10;
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                                                                                             Gardner, M.J.
Gardner, M.J.
Direct Submission
Submitted (02-NOY-1998) The Institute for Genomic Submitted Trive, Rockville, MD 20814, USA
                                                                                                                                                                                                           Plasmodium falciparum 3D7.

Plasmodium falciparum 3D7.

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 14867)

Gardner, M.J., Tettelin, H., Carucci, D.J., Cummings, L.M., Aravind, L.,

Sonin, E.V., Shallom, S., Mason, T., Yu, K., Fujii, C., Pederson, J.,

Shen, K., Jing, J., Aston, C., Lai, Z., Schwartz, D.C., Pertea, M.,

Salzberg, S., Zhou, L., Sutton, G.G., Clayton, R., White, O.,

Smith, H.O., Fraser, C.M., Adams, M.D., Venter, J.C. and Hoffman, S.L.

Chromosome 2 sequence of the human malaria parasite Plasmodium
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                                                                                                                                                                                                Science 282 (5391), 1126-1132 (1998)
                                                                                                                                                                                                                                                                                                                                                                      complete sequence.
AE001398 AE001362
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                                                                                                                                                                    (bases 1 to 14867)
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complement(1570./gene="pfB0490c"
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/Chromosome="2"
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                                           TTTTGGTTCTGGATTAGGTTTATTTGATCATAATTACATGCATCATTTCTTTGATTACTA
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CFAKFHENVDHIDNEKILNLIGLYVDNSILDIDINNKHCNINNLINENIEXISKLL
VEYGTIKUNDHIDNEKILNILGLYVDNSILDIDINNKHCNINNLINENIEXISKLL
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NISKLFISLSNSKYTCEVNENLLESLOSEFEKVTKTSKKGGLYHMDNNLLDNNSCE
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KKILYIANNILMYEMKGYYCEMLERVLSSHKEQNLFSYNYNKNVEHKMFDKILCHISE
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NNYKLNYEKSNNSNGNISNILKDDKNKNHNNVEMDLIDNKNENKKIQEKGQNGENCEN
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FILNKIIDKNFILFYECLLKILLNIKFVNFQSLCISLISLKNIYYNILRNNYYIVNNV
LFNDIMKFSLYLCNIFIGKRIKTENENAVLIIHNNDQTNYSNKENIKDIIIQKRIKEY
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SSIFSKKRDSHKKGSSFRGREGFINRKSGSFKY VNRLIKUNYNNY KGRNFHNGR
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TVYTKRLNNYKTYSAPYKKFNNLNISLYRKNRTFALNTKRSKPVGTIKSSVPRKRIKK
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NRNSYKKYKDTYIYILNDLSFYYKYIKNNDRTKKKKNFFLLSSSMKELICKNILSVSN
RYIKHLHEEDNFDQKDQYVCSLTFLNNLFFDKIIHFHYIYNLMCHVYKTYNYFKCNKL
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/note="predicted
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/codon_start=1
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                  Homo sapiens BAC clone RP11-724016
AC093899 AC068884
AC093899.3 GI:18497265
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Submitted (12-JUN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
On Feb 5, 2002 this sequence version replaced gi:15625013.
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                                                                                                                                                                                                                                          University School of MO 63108, USA
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Direct Submission
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by This sequence was finished as follows unless otherwise noted: restriction digest

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D McPherson, Department of Genetics, Washington University, St. McPherson, Information about the map position of this sequence, see http://genome.wustl.edu/gsc ָ פ Louis

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa.K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pletter de Jong and coworkers at http://www.chori.org pBACe3.6

NEIGHBORING SEQUENCE INFORMATION: Actual start of this clone is at actual end is at base position 17 rt of this clone is at base is at base position 172816 position 1 of RP11-724016; of RP11-724016.

simple sequence repeat from base position

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ON Plasmodium falciparum MAL3P5, complete sequence.

N AL034556 AL008971 AL008972 AL008978 AL010141 AL010153 AL010162
AL010206 AL010210 AL139179

AL034556.3 GI:7711164

HTG; centromere; CTRP protein; initiation factor E4;
Plasmodium falciparum 3D7

ESPING/threonine protein phosphatase.
Plasmodium falciparum 3D7

EM Plasmodium falciparum 3D7

EM Plasmodium falciparum 3D7

EL (bases 1 to 86827)

AS Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T., Churcher, C.M., Craig, A., Davies, R.M., Devlin, K., Feltwell, T., Gentles, S., Gwilliam, R., Hamlin, N., Harris, D., Holroyd, S.,
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                                                                                                                                                                                                                                                                    GAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAAAT 2274
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JOURNAL REFERENCE
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On or before May 14, 2001 this sequence version replaced
On or before May 14, 2001 this sequence version replaced
91:2982535, 91:2982536, 91:2894454, 91:2982554, 91:2982562,
91:2894489, 91:2982572, 91:2982574, 91:4493931.
For more information about this sequence or the Malaria Project,
See http://www.sanger.ac.uk/Projects/P_falciparum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lawson,D., Bowman,S. and Barrell,B. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The complete nucleotide sequence of chromosome 3 of Plasmodium
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                                                                                                                /gene="PFC0575w, MAL3P5.1"
/note="predicted splice donor
PFC0575w (revised)"
                                                                                                                                                                                                                                                                                                                                                                                                                                DTYNDDDDVDYEKEBDLVICKNIDDYIYKNTIGMNKSLEEFKNOFIEQADIEFONFLS
NVNLDQHGRVKSNDENTKSTEHIKNKNTINKGYDELIQOQMENNFIKKNIDNNISND
ISNNBINIIKKKLNQSDEDINLTSDLIYERLRTKVLMYIOXIEYLKRKYQVDIIHO
YPIIKNEKTVLDLLNYGYKIVMSPDVDNSLFEKTKIDSIPNEKDKNNQMENQKNSKNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKSKKKRKKNLSIYINLFICTLIYFTYCMCLLIKYISHLCIFFFFFFCFFLCYNILER
IYEECVGDLIRKKIERYNLYCEKKKIKFHMKDAIKKMEINMKDDDLYFNYHYDELLRC
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NINNLTRIKQVTHKKKSNEFTKENIKQILLHCVFSKIDFKIINNLSYIIKHFQMSNIT
VHSILNQISEKVKEKKDAENYLALHLFLLKDENITLESMMHIMDFFKSKQKVIECIRD
                                                                                                                                                                                                                       (revised
                                                                                                                                                                                                                                             /gene="PFC0575w, MAL3P5.1"
/note="predicted splice ac
                                                                                                                                                                                                                                                                                                                                       /gene="PFC0575w,
/note="predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="Hypothetical protein,
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/note="ppC0575w (MAL3P5.1), Hypothetical protein, len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(322. .603,826. .1023,1197. .1301,1458.
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splice donor sequence
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                      /note="potential
PFC0581w"
                                                                                               8107.
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percoselw"
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LKVKDEEIVSKKNNFSFSALSNDSNSVYKKIDTVNASFOWAQSPEXIFLNIKESHRWSSPGA
TLKKEKKKIWNRLLLSKEKYPNWQVWMDMKEKRIHIITFVTINLFFLLSLSHRYHDSV
TLKKEKKKIWNRLLLSKEKYPNWQVWMDMKEKRIHIITFVTINLFFLLSLSHRYHDSV
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FYDHINSSSNRCSFKNLKKQOTDDNTKHIIMGKEY PRINKSDEBEKNNNTCGNINIEK
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NNNNICSNNNNNICSNNNNNICSNNNDHICSNKHDEFCDDXFFKRKFKRI
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PFC058
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                                                                                                                                                                                                       PFC0581
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9369. .9505,9613. .9838)
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KNTNISSYSTYNNMEKENINIYDKYNIHNFYTEKSISYKDENCQHITLNMIYLLNQTY
DNICRICLNTNTNIYLNFYMINILKYICYKNMEIILLNYNHIEDMKKKINQKNNTNTS
                                                                                                                                                                                                                       /note="potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tentative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MLGLKRKNVFYLLVSVPSLFAYFLKRHKDNENNYETLINNNDIE
KIKKIRIHNKCSYIPLLFLNIYDSYIYKNKILRWLYFKFRKRKDKEEYYYITNMVRK
KRREAIKYNFISDEONLFNKFYIYEIVLEYSLKYGILSPHLSLYILKNISEHCVNIYP
                       'note="potential
                                                                                                                          'note-"potential
                                                                                                                                                     'gene="PFC0581w"
                                                                                                                                                                                                                                                          /gene="PFC0581w"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="PFC0581w"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="PFC0581w, hypothetical protein,
revised: new gene prediction, splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YSYDTMVNSFTFSYFFFSLSYLLFILFYHPDMYASYIFFKTLTYSGLPTYYYSLYNNI
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LYTQRIQNCCDIFSYIYKKYNFNEKNPFLNYLYYELHYIVYSEKKKKKFFSFISSSP
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/protein_id="CAB38968.]
/db_xref="GI:4493932"
                                                                             .8063
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8,8568. .8641,8713. .8812,8924. .9006,9122.
                       splice acceptor sequence for
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.8301

splice donor sequence for exon

4

of

* 10 A	38899 155 38959 215 39019	A.0%; Score 127.8; DB 3; Length 86827; Best Local Similarity 44.0%; Pred. No. 1:1e-09; Matches 1051; Conservative 0; Mismatches 1307; Indels 29; Gaps 11; Qy 35 TACAATATAAATTTCGTGTTTCTGGTTATTCTGTTCACATGATTTGGTTCTCAA 94	sc_feature s	/gene="pFC0581w" /note="potential splice acceptor sequence for exon 8 of PFC0581w" misc_feature 9007. 9012 /note="pFC0581w" /note="pFC0581w" misc_feature 9112. 9121 /gene="pFC0581w"	/gene="pF00581w" /note="ptential splice acceptor sequence for exon 7 of misc_feature 8813. 8818 /gene="pec0581w" /note="potential splice donor sequence for exon 7 of misc_feature 8913. 8923	misc_feature	/gene="PFC0581w" /note="potential splice acceptor sequence for exon 5 of PFC0581w" misc_feature 8369. 8374
Qy 1354 TGGGACCGTATGTTACGATCACTGCAAATATCATTCTTGGTTGG	11	CATAAAGCATAAAGGACCCGTTCAAGCTATTATACAAAGTTACAAACTGAATATAGCTT	OY 934 TGATATATCACAAAACAATTGTCTGGGACCATTTGAAATAAACTTTTTCTCAAACATTAC 993		394 7	Qy 515 TAAATTAAATACGAGGTGTGAATAT-CCGTTTATCGATCACTCCAATCATATATATTATAT	QY 455 TTTGATTACTATGAAGATTTTCTTACCAATTAAAATTTCGAATTCATATCTCTTGATTAT 514

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                                                                                                                                                                                                                                                                                                            Homo sapiens chromosome 18 clone CTD-2146H24 map 18, SEQUENCE, 4 ordered pieces.
           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 133877)
                                                                                                                             Homo sapiens
                                                                                                                                                                                                           HTG;
                                                                                                                                                                                                                                                                                 AC120883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAAAATGTAACCCTTTTACT----CATAGATTAATTACCGTATGTTTTTTGTTGCCATAA 1827
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                                                                                                                                                                                                   HTGS_DRAFT;
                                                                                                                                                                                                                                                                                                                                                                                           133877 bp
                                                                              Craniata; Vertebrata; Euteleostomi;
                                              Catarrhini; Hominidae; Homo
                                                                                                                                                                                                   HTGS_FULLTOP
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WORKING DRAFT
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E 3 (bases 1 to 13387)

RS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, P., DeArellano, K., Dewar, K., Dlaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Ngyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., Vo, A., Wilson, J., Wu, X., Wyman, D., Young, G., Zainoun, J., Viel, R., Vo, A., Wilson, J., Wu, X., Wyman, D., Young, G., Zainoun, J.,
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Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Weil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 6, 2002 this sequence version replaced gi:20531967. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zembek,L., Zimmer,A. and Zody,M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkly,L.,
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Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 132654 bases at least Q40 Consensus quality: 132863 bases at least Q30 Consensus quality: 132865 bases at least Q20 Consensus quality: 133065 bases at least Q20 Insert size: 13300; agarose-fp Insert size: 133577; sum-of-contigs Quality coverage: 17.1 in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                       Center project Information Center project name: L26769 Center clone name: 2146_H_24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center
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                               source
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                                                                                                                                                                                                                                                                                                                                                * This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 11 816: yap of 100 bp

* 1487: contig of 716 bp in length

* 1488 1587: yap of 100 bp

* 1984 2093: yap of 100 bp

* 1994 2093: yap of 100 bp

* 1994 2093: yap of 100 bp

* 1994 13877: contig of 406 bp in length

* 100 4 13877: contig of 131784 bp in length

* 100 4 13877: contig of 131784 bp in length

* 100 4 13877: contig of 131784 bp in length

* 100 4 13877: contig of 131784 bp in length
                                                 GAGTGTGAATATCCGTTTATCGATCACTCCAATCATGATTATGATTCTTGTGCTAATCCA 586
                                                                         GAAGATTTTCTTACCAATTAAAATTTCGAATTCATATCTCTTGATTATTAAATTAC
                                                                                                                  TTGGTTCTGGATTAGGTTTATTTGATCATAATTACATGCA-TCATTTCTTTGATTACTAT 466
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/note="assembly_fragment"

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24268 c 24460 g 43475 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="CTD-2146H24"
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/map="18"
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/db_xref="taxon:9606"
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                                       TTAATCTTGTTTCTTCCTACGGTATAAATATTAATCATCGAGGTAAAAAAAGTTTTGTCT 1726
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                                                                                  TGCATCTTTAACATATTTATTGTTAGTTGGAATTTAATAAGAGCGAACTTGTAACATTAC 1606
                                                                                                         TACGATCACTGCAAATATCATTCTTGGTTGGTCAACAATAAAAACAAAAAACAAGAAAAAAA 1426
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                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                           ORGANISM
                                                                                                                           AUTHORS
                                                                                                                                                                                                                               Plasmodium falciparum MAL3P5, complete sequence. AL034556 AL008971 AL008972 AL008978 AL010141 AL0 AL010206 AL010210 AL139179 AL034556.3 GI:7711064 HTG; centromora.
 Bowman,S., Lawson,D., Basham,D., Brown,D., Chillingworth,T., Churcher,C.M., Craig,A., Davies,R.M., Deviln,K., Feltwell,T., Gentles,S., Gwilliam,R., Hamlin,N., Harris,D., Holroyd,S., Hornsby,T., Horrocks,P., Jagels,K., Jassal,B., Kyes,S., McLean,J., Moule,S., Mungall,K., Murphy,L., Oliver,K., Quail,M.A., Rajandream,M.-A., Rutter,S., Skelton,J., Squares,R., Squares,S., Sulston,J.E., Whitehead,S., Woodward,J.R., Newbold,C. and Barrell,B.G.
                                                                                                                                    Plasmodium falciparum 3D7.
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 86827)
                                                                                                                                                                                                      HTG; centromere; CTRP protein; initia Serine/threonine protein phosphatase.
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The Sanger Centre, Wellcome Trust Genome Campus, Hinxton,
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For more information about this sequence or the Malaria Project,
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complement/375'
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NVNLLQHGRVKSNDENTKSTEHIKNKPTINKGYDELLIQNQMENNFIKKNIDNISH
ISNNEINIIKLKKLNGSDEDINITSDLIYERLEFKVLMYIQKIEYLKFKYQYDIINEQ
YPIIKNEKTVLDLLNKGYKIVMSPDVDNSLFEKTKIDSIPNEKDKNNQMENQKNSKNY
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IKSKKKRKKNLSIYINLFICTLIYFTYCMCLLIKYISHLCIFFFFFFCFFLCYNILER
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hexExon"
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1097 aa, possible signal sequence, predicted usin
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/note="predicted splice acceptor
(revised of PFC0575w)"
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KNTNISSYSTYNNMEKENINIYDKYNIHNFYTEKSISYKDENCQHITLNMIYLLNQTY
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PFC0581w"
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3 3 7C AC105425 205130 bp DNA linear HTG 15-JAN-2002 N Homo sapiens chromosome 7 clone RP11-776N17, WORKING DRAFT SEQUENCE, 12 unordered pieces. N AC105425. N AC1	1724 TCTTATTTCGGGATGCAGGATGAACCTAATGCTTTAATTTTTTAATATATAT

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FEATURES
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Consensus quality: 198378 bases at least Q40
Consensus quality: 199330 bases at least Q30
consensus quality: 200198 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality coverage: 10.60 in Q20 bases; agarose-fp
Quality coverage: 10.87 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
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Insert size: 203204; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Washington University Genome Sequencing Center
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                                                                /note="assembly_name:Contig110
                                                                                                                                 /note="assembly_name:Contig108
                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
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   'note="assembly_name:Contig111"
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of 2013 bp in length
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                                                                                              TAACGATTGTGAAAAATATTTTATTTGTTAGCTGATCTCAATATTATGTTCCAGGTA--- 844
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                            TTCTCTCACAATCAATATCGACCCTATTTGGATTTTCTGGATATTCGTTAAAATTTGCGA
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82414. .122098
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Submitted (28-JUN-1994) Laurie S. Kaguni Ph.D. Dept. of Biochemistry, Michigan State University, East Lansing, !
                                                                                                                                                                                                                                                                                                                                                                                                                                               Lewis,D.L., Farr,C.L., Farquhar,A.L. and Kaguni,L
Sequence, organization, and evolution of the A+T
Drosophila melanogaster mitochondrial DNA
Mol. Biol. Evol. 11 (3), 523-538 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitochondrion Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 4601)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitochondrial DNA;
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Mitochondrion Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 12511 to 12682)
     Drosophila
                                                                                                                Clary, D.O., Wahleithner, J.A. and Wolstenholme, D.R. Transfer RNA genes in Drosophila mitochondrial DNA: related
                                                                                                                                                                                     Drosophila mitochondrial DNA: a novel Nucleic Acids Res. 10 (21), 6619-6637
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Lewis, D.E., Farr, C.L. and Kaguni, L.S.
Drosophila melanogaster mitochondrial DNA: completion
nucleotide sequence and evolutionary comparisons
Insect Mol. Biol. 4 (4), 263-278 (1995)
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Lewis, D.L., Farr, C.L., Farquhar, A.L. and Kaguni, L.S.
Sequence, organization, and evolution of the A+T reg
Drosophila melanogaster mitochondrial DNA
Mol. Biol. Evol. 11 (3), 523-538 (1994)
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Ballard, J.W., Olsen, G.J.,
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Analysis of nucleotide substitutions of mitochondrial
Drosophila melanogaster and its sibiling species
Mol. Biol. Evol. 4 (6), 638-650 (1987)
                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                          Lewis, D.L., Farr, C.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 258 (5086),
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Proc. Natl. Acad. Sci. U.S.A. 87
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                                                                                                             /product="tRNA-Gln"
171. .239
                                                                                                                                                                                  /note="derived from new and previously submitted
sequences; sequence is a composite containing se
obtained from different Drosophila melanogaster
           /product="NADH dehydrogenase
/protein_id="AAC47811.1"
/db_xref="GI:1166530"
                                                                                                 /product-"tRNA-Phe"
                                                                                                                                                         /product="tRNA-Ile"
                                                                                                                                                                                                                                           /organelle="mitochondrion"
                                                                                                                                                                                                                                                                                     Location/Qualifiers
translation="MFNNSSKILFITIMIIGTLITVTSNSWLGAWMGLEINLLSFIPL"
                                                         transl_table=5
                                                                      codon_start=1
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ALIGDDQIYNVIVTAHAFIMIFFMVMFLMIGGFGNWLVPLMLGAPDMAFPRMNNNSFW
LLPPALSLLLVSSMEURGAGTGWTVEPPLSAGIAHGGASVDLAIFSLHLAGISSITGA
VNFITTVINMRSTGISLDRMPLFVWSVVITALLLLLSLPVLAGAITMLLTDRNLNTSF
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LAIGLLGFIVWAHHMETVGMUYDTRAKETSATMIIAVPFGIKIRSWLATLHGTQLSYS
PALIMALGFVFLFTVGGLTGVVLANGSVDILHDTYYVVAHFHYVLSMGAVFAIMGF
IHWYPLFTGLTLNNKWLKSHFIIMFIGVNLTFFPQHFLGLAGMPRRYSDYPDAYTTWN
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IMMMSTLITLFFYLRICYSAFMMNYFENNWIMKMNMNSINYNMYMIMTFFSIFGLFLI
                                                                                                                                                                /product="ATPase 6"
/product="ATPase 6"
/protein_id="AAC47815.1"
/protein_id="AAC47815.1"
/db_xref="GI:1166534"
/translation="MMTNLFSVFDPLAIFNFSLNWLSTFLGLLMIPSIYWLMPSRYNI
/translation="MMTNLFSVFDPLAIFNFSLNWLSTFLGLLMIPSIYWLMPSRYNI
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LFFNNYVNRFLLHGQLIEMIWTILPAIILLFIALPSLRLLYLLDEINEPSVTLKSIGH
QWYWSYEYSDFNNIEFDSYMIPTNELMTDGFRLLDVDNRVVLPMNSQIRILVTAADVI
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/protein_id="AAC47813.1"
/db_xref="GI:1166532"
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/note="TAA stop codon
residues to the mRNA"
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/protein_id="AAC47812.2"
/db_xref="GI:7412849"
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LKSGAAPFHFWFPNMMEGLTWMNALMLMTWQKIAPLMLISYLNIKYLLLISVILSVII
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                                                                                                              MWNSILLTLHKEFKTLLGPSGHNGSTFIFISLFSLILFNNFMGLFPYIFTSTSHLTLT
LSLALPLWLCFMLYGWINHTQHMFAHLVPQGTPAILMPFMVCIETISNIIRPGTLAVR
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/product="ATPase 8"
/protein_id="AAC47814.1"
/db_xref="GI:1166533"
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3907. .4068
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/transl_table=5
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AATTATCAAAGAGAATAAGAGATGACAACCAAAAGGTTGTGGAATAATGGTCCCTGCC--
                                                                 TCGATCACTCCAATCATGATTATGATTCTTGTGCTAATCCAGCAAATTATTAACAAGAGT 605
                                                                                                                                                                                                                                                TTTTAAAAAATAAACAAAAAATTTTTAATAAATAAATTTTATAATGAAATATAATTTAT 17656
                                                                                                                                                                                                                                                                                                                                           TTTTAAAAATTTCTTAAATGTATTATTTTTATAAAAATATTTATATAAAAATCATGT
                                                                                                                                                                                                                                                                                                                                                                                   TATTTGATCATAATTACATGCATCATTTCTTTGATTACTATGAAGATTTTCTTACCAATT 485
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATATATAGAAAAATTA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAAAAAAACAAACAAACCCCCCCCCCCGATATAGTTTTTTGGTTCTGGATTAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTAAATCAAAAAGAGTATTGATTGAAGTGTAAACATATTTCGTTATGACCCCCAAAAAA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATTCCATTTGGTTGGATTACACAGTTAAGTTTTTGTGTTTCTTTTTTGTGTATATGTATATGT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATTTTTAAATTTAATAATAAATAAATTTAATAATTAATTAAATAAATAAATCTATTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCATTTAAAATATTTACAAGTAATTAATTATCTTTACATTGTATTGTTATAACAAAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTCACATGATTTGAGTTTGGTTCTCAATTTGGATTCCAAGATAATTAAATATTAAAAT
                                                                                                                                                           ATTGAGAAAAAACCGAAAATAAGAAAAAGGGAAAGAGTAGTGACCCATGGAGTATGTGAAT 665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="tRNA-Asn"
6184. .6251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="tRNA-Arg"
6119. .6183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="NADH dehydrogenase subunit 3"
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PKSSSRLPFSLRFFLITIIFLIFDVETALILPMIIIMKYSNIMIWTITSIIFILILLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="tRNA-Gly"
5608. .5961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLGNIITILIVYQWWRDVSREGTYQGLHTYAVTIGLRWGMILFILSEVLFFVSFFWAF
FHSSLSPAIELGASWPPMGIISFNPFQIPLLNTAILLASGVTVTWAHHSLMENNHSQT
TQGLFFTVLLGIYFTILQAYEYIEAPFTIADSIYGSTFFMATGFHGIHVLIGTTFLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAC47816.1"
/db_xref="GI:1166535"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYHEWNQGMLNWSN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLLRHLNNHESKNHHEGFEAAAWYWHFVDVVWLFLYITIYWWGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="tRNA-Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tRNA-Ala"
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Pred. No. 4.6e-09;
0; Mismatches 1276;
                                                                                                                                                                                                                                                                                                                                                                                                                                   - AATTATTTAAATAATTTAATATAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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37;

Gaps

245

185

17253 125

17313

425

17491

17536

17596

1786 18915	727 TATTITTCGCGATGCAIGAAGGATAAACCTAATGACTTTAATTTTTTGAAAATGTAACCCT 1	17 188
1726 18856	67 TTAATCTTGTTTCTTCCTACGGTATAAATATTAATCATCGAGGTAAAAAAAGTTTTGTCT	16 187
1666 18796	607 AATATTTATATTAGATACTAGTATGTGATTATTCCAAATACATAC	16 187
1606 18736	47 TGCATCTTTAACATATTTATTGTTAGTTGGAATTTAATAAGAGCGAACTTGTAACATTAC 1	15 186
1546 18676	.488 AGTTTCGAAGTCCTCTACAAGCGTGTAACCATCTGCAACTATTAAATTGCTTTCT-TTAA 1 	14 186
1487 18616	.428 GAAAACGATTITTCTTGGATTCCATTCAATGATCTAAAATGCATAGATCTTTTGGGTTAC 1	14 185
1427 18556	368 ACGATCACTGCAAATATCATTCTTGGTTGGTCAACAATAAAAACAAAAACAAGAAAAAA 1 	13 184
1367 18496	311 ATGTGATGTCGATAAATGAAATTCACACGCGGTGGTAATAATTATGGGACCGTATGTT 1	13 184
1310 18436	251 ATCCATATATGGGTATGCTATACCTTTCACGTATGCTATACTAGAGAGACTAAAGAATAGTT 1 	12 183
1250 18376	1191 TTAGTGGTCAACATAATACATAATTCCTTACAGAAAAAACAAAC	11 183
1190 18316	1131 TTTGGAATTACCGGTTGTTATGTAAATATAGATTTAGTGGTAAACAAATATGTTAATCAA 1 	11 182
1130 18256	.076 CAAGCTATTTATACAAAGTTACAAACTGAATAGCTTGAAATCCTTTAGAAAAT 1 	107 1819
1075 18196	1016 AAATACGATTTTACAGCGTCACTAGTTGAGATTACTAGCATAAAGCATAAAGGACCGTT 1	10 181
1015 18136	956 CTGGGACCATTITGAATAAACITTTTCTCAAACATTACGGGACACTGGACTCGACCCTTA 1	180
955 18076	901 TAACTATATATTATCGCGGATATATGATAACAATGATATATCACAAAACAATTGT 9	180
900 _. 18016	841 GGTATTTGCATAATCTTCTGTTTAAAGCATATTTTGTCTTTTTTTT	179
840 17956	784 GCGATAACGATTGTGAAAAATATTTTATTTGTTAGCTGATCTCAATATTATGT-TCCA 	178
783 17896	724 AGCTITCTCCACAATCAATATCGACCCTATTIGGATTTTCTGGATATTCGTTAAAATTT	7 178
17836	17777 ATATATCTAATAATTTAAATAAAAATTTTAAAATTTAAAAATGTAGATATAATTTATAA :	177

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Search completed: June 11, 2003, 01:50:10 Job time: 8545.25 secs

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Result
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
         000
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                        3202
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1: /SIDS2/gcgdata/g;
2: /SIDS2/gcgdata/g;
3: /SIDS2/gcgdata/g;
4: /SIDS2/gcgdata/g;
5: /SIDS2/gcgdata/g;
5: /SIDS2/gcgdata/g;
6: /SIDS2/gcgdata/g;
8: /SIDS2/gcgdata/g;
9: /SIDS2/gcgdata/g;
9: /SIDS2/gcgdata/g;
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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3202
1 atgtgggtattatattgttg.....gagagagagaaactagctcc 3202
      100.0
2.0
2.66.6
2.66.6
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                                                                                                                                                                                                                                                                                                                           Query
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Listing first 45 summaries
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0. / SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986_DAT: *

1. / SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990_DAT: *

2. / SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990_DAT: *

2. / SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991_DAT: *

2. / SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991_DAT: *

3. / SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991_DAT: *

4. / SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991_DAT: *

5. / SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994_DAT: *

6. / SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994_DAT: *

7. / SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997_DAT: *

7. / SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999_DAT: *

9. / SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999_DAT: *
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
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ABL32890
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9837.455 Million cell updates/sec
                        DNA transcription
Human immune syste
Human immune syste
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DNA transcription
                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                     DNA encoding a cyt
Human breast cance
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pretrea
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2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	٠	•	•	٠		•	•	•	٠	2.5	
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Query Match Best Local Similar Matches 3202; Con Y 1 ATGTGG Y 1 ATGTGG Y 61 TATTCT G1 TATTCT HILL HI	The present sequence encodes a DWF4 polypeptide. The polypeptic cytochrome P450 enzyme that mediates multiple steps in synthes brassinosteroids. Specifically, it mediates multiple 2alpha-hydroxylation steps in brassinosteroid biosynthesis. The polynucleotide is used for altering the phenotype of a plant. I plants display a dramatic reduction in the length of different and this size reduction is attributable to a defect in cell element of the DWF4 polynucleotides and polypeptides can be used in diagnous assays and to generate antibodies, which can be used to product immunogenic compositions. Sequence 6888 BP; 2294 A; 1010 C; 1193 G; 2391 T; 0 other;	new isolated dwid polynucieotide userul plants, for diagnostic assays and in the Claim 3; Fig 10A-G; 113pp; English.	(0	(ARIZ-) ARIZONA BOARD Azpiroz R, Choe S,)	FEB-1999; FEB-1999;		3'UTR WO200047715-A2.	intron	intron	intron	exon	exon	intron	exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells.
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acute myeloid leukaemia; Alzheimer's disease; AIDS; epile
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                                                          GTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTGGGACAACAATGAA
                                                                                                                                                                        TTTTTTATG----GAACAAGAAATAACAGATAGAAAACTATTTTGTTGTAGGAATGGAAG
                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Pred. No. 0
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06-APR-2000; 07-APR-2000; 30-JUN-2000;

2000DE-1019058. 2000DE-1019173. 2000DE-1032529. 2000DE-1043826.

06-APR-2001; 06-DEC-2001

2001WO-EP03973

01ek

(EPIG-) 01-SEP-2000;

EPIGENOMICS

AG

Berlin

WPI;

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ABK28127 4
ABK28127
ID ABK2
XX ABK2
XX ABK2
AC ABK2
XX DNA
XX DNA
XX DNA
XX PNA;
KW PNA;
KW PNA;
KW Angul
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XX O06-D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK28257
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New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid

Claim 1; SEQ ID No 131; 32pp; English

chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer, in particular an oligomerical preptide nucleic acid (PNA)-oligomer that hybridises to or is identical to the chemically pretreated DNA of genes associated with DNA transcription. The set of oligomer probes are useful for detecting the cytosine methylation state and/or single nucleic acids are useful for diagnosing or treating diseases associated with DNA transcription (particularly with the methylation status), e.g. adenosine deaminase deficiency, viral infection, retroviral infection, Sezary syndrome, tuberculosis, developmental disorders, provisals, Rieger's syndrome, neurological disorders, neurodegenerative disorders, Waardenburg syndrome, Niemann-Pick disease, myelodysplastic syndrome, monacital heart infection, broattenion and opened a pretrocate of a protection of the consolidation infarction, hypertension, angiogenesis, erythropoiesis, congenital heart disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours or cancer. Sequences ABK28127-ABK28472 represent DNA transcription associated genomic The invention relates to a nucleic acid, which comprises a segment of the d genomic DNA molecules of the invention sequence data for this patent did not for torm part of printed

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AC ABL3
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Huma
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Matches
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  Human;
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                                                                                                              ABL32890 standard; DNA;
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                                                                                                                                                                                                              GTAATATACATTAAGCAAATTTTAAAAAA 2273
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                                                                                                                                                                                                                                                                                                                       GTCAATAACAATGCATAGAAAGTTCCAAAAAAAATTTTGTTAACAGAAACTTCCAAATTT
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                           system associated gene SEQ
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Pred. No. 0.
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cytosine methylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6131 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          macular degeneration, arteriosclerosis, anaemia, cancer acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 863; 32pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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 428
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                                                                     GTTGCCATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTTCTGCAAATAT-TAAAT
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                                                                                                                                                                                                                                                                                TAGGAATTCAATGCTACTATCAATAGAAGAAACAGCTGAGTATTACATTTTAATTTAAAG
                                                                                                                                                                                             CATCGAGGTAAAAAAAGTTTTGTCTTATTTTCGCGATGCATGAAGGATAAACCTAATGAC
                                                                                                                                                                                                                                                                                                AATAAGAGCGAACTTGTAACATTACAATATTTATATTAGATACTAGTATGTGATTATTCC
                                                                                                                                                                                                                                                                                                                                     Piepenbrock
 TATAGTTTTAGTGGTATTTTTTTTTTAAATTATAGTGTAATATTTAAGTGTTTTTAAAAT
                                                       TAGATTTATTAAAGATTTTTTATTGTTTGTAAAATAATTTGTAAGTTTTTGATTTGGAAT
                                                                                                                                                                                                                          invention provides a number of human immune system associated are modified by the methylation of cytosines. The sequences
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                2130 A; 39 C; 1018 G;
                                                                                                                                                                                                                                                                                                                                                                                                       2.68;
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                                                                                                                                                                                                                                                                                                                                                                                          Score 82.8; DB 24;
Pred. No. 0.00029;
0; Mismatches 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                2944 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      German
                                                                                                                                                                                                                                                                                                                                                                                                                                                 other;
                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene, useful
abnormal
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16;

6

1876

1817

1701

247

1641 187

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RESULT 6
ABL32426
ID ABL32426
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XX ABL3
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                                                               Olek A,
                                                                                                                              30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                 (EPIG-)
                                                                                                                                                                                    02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                      Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirhemmatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                 WO200200928-A2
                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                  neurofibromatosis; rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune system associated gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL32426 standard;
                     2002-130909/17
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                                                                                             EPIGENOMICS
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                                                         Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATAAAGAAAAATAGTAAAAATAATATATTTGAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAAAAAGGGAAATAAAAATATTTAATTGACGTTAGTTATTAGTTTTTGAAAAAAGGTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATTITTTTATGTTTTGAATTTTTTTATAATAGATTTTTTGTAGTTTTGAAAAGTATTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATGGATTTTTTTTAATATAAATTTAT--ATTTTTATTTTTTAAATTTTTAAATTTTTA
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                                                                                               ĀG
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                                                       Berlin
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                                                                                                                                                                                                                                                                                                                                            psoriasis; bowel dis
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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
1625 TAGTATGTGATTACTTCCAAATACATACTTTGGATGTTTAAACTTAAATCTTGTTTCTTCCT
                                                                                                                                                                                            374;
                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                            9810 BP; 2770 A; 79 C; 1978 G; 4983 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          methylation
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                              2.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32pp + Sequence Listing;
                                                                                                                                                                           0;
                                                                                                                                                                                                                   Score 82.6; DB 24
Pred. No. 0.00031;
                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                DB 24;
                                                                                                                                                          404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune system associated ytosines. The sequences
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                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                           9810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acute myeloid
                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders,
                                                                                                                                        Gaps
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2266 1422 1362 1302 1242 1122 TTTTATAATTTATATATATATATATGTTTATATGTATAATTTATTGTATATGTTTATATAT 1685 AATGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGAATTAAAATATTAACTTT 2385 ATAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATT ATTAATATTTTTTGAAATCTACAAATTATTAATATTTAGTCAATAACAATGCATAGAAAG TTTATATTTAGTTATAAATACATTATGAACCAATAATAGTTGGTGAATTCAAATATCTCC AACAATATTAATAAAATATGATGCCTATAATGTATTTCCTATGTTCTTAAAATATTTTTT 2026 CATTTTAATTTAAAGACAAAATTTTTGAAAA.------ATGTTATAATTTCT 1966 CTGCAAATATTAAATTAGGAATTCAATGCTACTATCAATAGAAGAAACAGCTGAGTATTA 1921 ATTACCGTATGTTTTTGTTGCCATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTT ACGGTATAAATATTAATCATCGAGGTAAAAA----AAGTTTTGTCTTATTTTCGCGATGCA TGAAGGATAAACCTAATGACTTTAATTTTTTGAAAATGTAACCCTTTTACTCATAGATTA 1481 2325 1421 2205 2086 1181 1861 1001 1741 1684

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RESULT 7
AAS45388/c
ID AAS45388 s
XX AAS45388;
XX AAS45388;
XX AAS45388;
XX Call cycle
KW human impu
KW graft-vers
KW arthritis;
KW immunosupp
KW PCR primer
XX Homo sapie
PN W020016891
XX 15-MAR-200
PR 06-APR-200
PR 07-APR-200
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                                                                  Query Match
Best Local
Matches 45
                                                                                                                                                                                                             Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAR-2000;
06-APR-2000;
07-APR-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Designing primers and probes for analysing diseases associated cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified ge associated with cell cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 93; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic; immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cycle; human; CpG dinucleotide;
immunodeficiency virus; neurodo
                                                                                         Similarity
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  AACAATAAAAACAAAAACAAGAAAAAAAAAAAAAGAATTTTTCTTGGATTCCATTCAATGA
                                                                                                                                                       15732
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; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
                                                                     Conservative
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                                                                                                                                                       BP;
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                                                                                                                                                     4638 A;
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                                                                                    2.6%;
43.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berlin
                                                                                                                                                     70 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1618
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                                                                  0;
                                                                                    Score 82.6; DB 22; Pred. No. 0.00032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽P
                                                                     Mismatches
                                                                                                                                                                                                  and cancers.
                                                                                                                                                     2672 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytosine
                                                                                                                                                   8352 T; 0 other;
                                                                  574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methylation; HIV;
                                                                  Indels
                                                                                                           Length
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CC The invention relates to a nucleic acid, which comprises a segment of the CC chemically pretreated DNA of genes associated with DNA transcription from CC one of 346 sequences, and an oligomer; in particular an oligonucleotide CC or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical to the chemically pretreated DNA of genes associated with DNA cytosine methylation state and/or single nucleotide polymorphisms (SNPs) cytosine methylation state and/or single nucleotide polymorphisms (SNPs) diagnosing or treating diseases associated with DNA transcription CC (particularly with the methylation status), e.g. adenosine deaminase cytosical disorders, immunological disorders year syndrome, comerculosis, developmental disorders, psoriasis, Rieger's syndrome, cytoberulosis, developmental disorders, psoriasis, Rieger's syndrome, construction, hypertension, anglogenesis, erythropolesis, congenital heart cytoberulos, cyto
                                                                              Query Match
Best Local S
Matches 453
                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, sol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID No 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EPIG-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PNA: Cytosine methylation state; SNP; retroviral infection; gene; ds; single nucleotide polymorphism; adenosine deaminase deficiency; cancer; viral infection; Sezary syndrome; haematological disorder; cancer; immunological disorder; Werner syndrome; developmental disorder; tuberculosis; psoriasis; Rieger's syndrome; aurological disorder; erythropoiesis; myelodysplastic syndrome; mardenburg syndrome; retrovincesis; myelodysplastic syndrome; myocardial infarction; hypertension; arthritis; polyglutamine disorder; solid tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA transcription associated gene;
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                         Score 82.6;
Pred. No. 0
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RESULT 9
AAS45384/5384 standard; DNA; 56
XX
AC
AAS45384;
XX
DT
18-DEC-2001 (first entry:
XX
DEC chemically pretreated gene
XX
Cell cycle; human; CpG dir
KW draft-versus-bost disease;
KW arthritis; arterioscleros;
KW dramunosuppressive; antitum
XX
PCR primer.
XX
PD
20-SEP-2001; 2001WO-EP029;
XX
PD
15-MAR-2001; 2001WO-EP029;
XX
PD
07-APR-2000; 2000DE-10138;
PR
06-APR-2000; 2000DE-10191;
PR
07-APR-2000; 2000DE-10191;
PR
07-APR-2000; 2000DE-10438;
PR
07-SEP-2001; 2000DE-10438;
PR
07-SEP-2000; 2000DE-10438;
PR
07-SE
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                                                                                                                                                          Query Match
Best Local S
Matches 285
                                                                                                                                                                                                                                                                                                                              Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or porgonosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of the parameters are useful for the diagnosis and therapy of the prognosis events which are disadvantageous to patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Designing primers and probes for analysing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes associated with cell cycle -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          graft-versus-host disease; g
arthritis; arteriosclerosis;
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                                                                                                                                                                                                                                                                                            HIV infection, neurodegenerative disorders, graft-versus-host ing, glomerular disease, Lewy body disease, arthritis,
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immunodeficiency virus; neurod
                                                                                                                                                                          Similarity
  TCAATGCTACTATCAATAGAAGAAACAGCTGAGTATTACATTTTAATTTAAAGACAAAAT
                                                                                                                 ATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTCTGCAAATATTAAATTAGGAAT
                                                                             2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                              solid tumours
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                                                                                                                                                                                                                                       207
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us; neurodegenerative disorder; solid disease;
glomerular disease; Levy body disease;
s; anti-HIV; neuroprotective; antiarthr
                                                                                                                                                            0
                                                                                                                                                        Score 81.6; DB 22;
Pred. No. 0.00044;
0; Mismatches 292;
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07-APR-2000;
30-JUN-2000;
                              Fragments genes and analysing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; tumour; CpG dinucleotic
                                                                                                                                                                                                                                                                                                              15-MAR-2000;
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                                                                                                                                                                                              EPIGENOMICS
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                                                                                                                                                        Piepenbrock
                                    oncogenes, useful in diseases associated w
                                                                             of chemically
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2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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ATAAAAAAATATTTAATAACGTTAAAAATATAAATATAT 1531
                              AAAACGGAATTAAAATATTAACTTTAAAATAAATAAAAAAT
                                                                                                                                                                            TTTTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAACTATTTTGTTGTGGAATGGAA
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chemically modified sequence

dinucleotide; oncogene; single-nucleotide polymorphism; antitumour; cytostatic; SNP;

modified genes associated with tumour suppressor eful in designing primers and probes for clated with cytosine methylation state e.g.

ID No 148;

27pp; English.

Ş 망 δÃ D Ş 밁 Qy В Ωy

 $x \neq 0$ CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CC concegence having a sequence taken from 536 (actually 533 since CC (ss) and sequences complementary to (ss). The nucleic acid may be a CC (ss) and sequences complementary to (ss). The nucleic acid may be a CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may CC and/or single nucleotide polymorphisms and also to be used in an CC carray for analysing diseases associated with CpG dinucleotides e.g. CC array for analysing diseases associated with CpG dinucleotides e.g. CC ascertaining genetic and/or epigenetic parameters for the diagnosis CC diseases, by analysing cytosine methylations. The predisposition to specific CC compared to another set of genetic and/or epigenetic parameters may be CC differences serving as basis for diagnosis and/or prognosis events which CC 33 genomic sequences derived from tumour suppressor genes and CC complementary sequences with even numbered Seq ID numbers are the CC iD 2 and ID1, ID 536 and ID 535, except for those whose partner sequence (e.g. is missing). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electron format directly from WIPO at Sequence 5689 BP; ftp.wipo.int/pub/published_pct_sequences. 1490 A; 207 C; 1277 G; 2707 T; œ electronic other,

Query Match Best Local 285; Similarity Conservative 2.5%; 49.1%; 0; Pred. Score 81.6; o . 0.00044; DB 22; Length 5689;

В Qy 밁 δÃ Ъ Qy B δÃ В δã 1810 1870 1930 2004 1990 1944 2050 TAGTCAATAACAATGCAT-AGAAAGTTCCAAAAAAAATTTTGTTAACAGAAACTTCCAAA AGTTGGT-GAATTCAAATATCTCCATTAATATTTTTTGAAATCTACAAATTAATAATATT TCAATGCTACTATCAATAGAAGAAACAGCTGAGTATTACATTTTAAATTTAAAGACAAAAT CCTATGTTCTTAAAATATTTTTTTTTATATTTAGTTATAAATACATTATGAACCAATAAT TTTTGAAAAATGTTATAATTTCTAACAATATTATTAAAATATGATGCCTATAATGTTTT 2181 1871 1811 2122 1931 2051 1991 1943

2361 AAAACGGAATTAAAATATTAAACTTTAAAATAAATAAAAA 2400 1750 1824 ATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTCTGCAAATATTAAATTAGGAAT 1883 TGTTATCTAGGTAGGTGTAATTAATA-ATGCATGGTGCGATTCAGAATTGGGACAACAATG GTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTCAAAGTA TTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAACTATTTTGTTGTGGAATGGAA **ТАТААЛАТАЛААТАЛАТАЛААЛАЛАТАТАТАЛАЛАЛАТАТАТАЛАЛАТАЛАЛАТАЛАТАТ** Mismatches 292; Indels ω Gaps 1691 2241

DЬ 1570 ATAAAAAAAATATTTAATAACGTTAAAAATATAAATATAT 1531

RESULT 11 ABK28226/c ID ABK282 ABK28226 ABK28226 standard; DNA; 5689 ВP

DNA transcription associated complementary 23-APR-2002 (first entry) genomic DNA #50

psoriasis; Rieger's syndrome; neurological disorder; erythropolesis; neurodegenerative disorder; Waardenburg syndrome; Niemann-Pick disease; myelodyspiastic syndrome; myecardial infarction; hypertension; arthritis; angiogenesis; congenital heart disease; HDR syndrome; gene therapy; PNA; cytosine methylation state; SND; retroviral infection; gene; ds; single nucleotide polymorphism; adenosine deaminase deficiency; cancer; viral infection; Sezary syndrome; haematological disorder; tuberculosis; immunological disorder; Werner syndrome; developmental disorder; DNA transcription associated gene; peptide nucleic acid;

Unidentified.

WO200192565-A2

06-DEC-2001.

06-APR-2001; 2001WO-EP03973

06-APR-2000; 2000DE-1019058 07-APR-2000; 2000DE-1019173 30-JUN-2000; 2000DE-1032529 01-SEP-2000; 2000DE-1043826

01ek EPIGENOMICS Piepenbrock ĀG Ç Berlin

(EPIG-)

WPI; 2002-090046/12.

New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, sol: disorders, Werner syndrome, tumours or cancer solid

Claim 1: SEQ ID No 100; 32pp; English

The invention relates to a nucleic acid, which comprises a segment of the CC chemically pretreated DNA of genes associated with DNA transcription from CC one of 346 sequences, and an oligomer, in particular an oligonucleotide corpeptide nucleic acid (pNA)-oligomer that hybridises to or is identical corpeptide nucleic acid (pNA)-oligomer that hybridises to or is identical corpeptide nucleic acid power probes are useful for detecting the CC transcription. The set of oligomer probes are useful for detecting the CC in a chemically pretreated genomic DNA. The nucleic acids are useful for CC diagnosing or treating diseases associated with DNA transcription corporated vith DNA transcription corporated infection, retroviral infection, searly syndrome, corporated disorders, immunological disorders, psoriated with DNA transcription corporated disorders, psoriatis, Reger's syndrome, corporated processes, myelodysplastic syndrome, myocardial corporated processes, arthritis, polyglutamine disorders, social tumours associated genomic DNA molecules of the invention.

CC Note: The sequence data for this patent did not form part of the printed corporated per printed disorders and directly from the corporate and patent office.

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RESULT 1
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ID ABL
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Best Local
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     02-JUL-2001;
                                                           03-JAN-2002.
                                                                                                                                                                                                                 gene;
                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune
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                                                                                                             WO200200928-A2
                                                                                                                                                              Homo sapiens
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, theumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                               Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; immune system disease; cytosine methylation; antiasthn antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anacute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy, neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; and the state of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JAN-2002
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                                                                                                                                                                                                                SEQ ID NO 864; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                  Piepenbrock
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bowel disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a gene (I) derived from Buchnera sp. containing the DNA (a) or (b), (a) has a fully defined base pair sequence selected from a table of sequences found in the Buchnera sp. genomic DNA of ABA92787 given in the specification or is a DNA selected from complementary DNA sequences, and (b) is a DNA which hybridises with the DNA (a) and encodes a protein. Also described are: (1) a recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 16-230; 237pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A genomic DNA of cockroach-symbiotic bacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 640681 BP;
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         GTCAAAGAAAATATTATTTTTCCTGAAAATGAATATAAATAGGACAATAACTGATTATTT
                                                                                                                                                                                          GCATGAAGGATAAACCTAATGACTTTAATTTTTTGAAAATGTAACCCTTTTACTCATAGA
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Pred. No. 0.00086;
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                                                            Olek A,
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Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cance antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                 Synthetic
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01-SEP-2000;
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Piepenbrock C,
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The present invention relates to chemically modified DNA sequences of condified using a solution of bisulphite, bydrogen sulphite or disulphite. Also disclosed are oligonucleotides and/or PNA oligoners of or detecting the cytosine methylation state (CPG islands) of these epigenetic parameters of genes associated with signal transduction. CC contain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine, ceyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, ceyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, cc sequences of the invention are useful for the diagnosis and therapy of cancer. ABK31158 ABK31545 represent chemically pretreated genomic DNA con be dead of the diagnosis and transduction, or their complementary sequences of the invention are useful for the diagnosis and therapy of cancer. ABK31158 ABK31545 represent chemically pretreated genomic DNA cc their complementary sequences associated with signal transduction, or contain transduction, or contain transduction, or their complementary sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.5%;
Best Local Similarity 44.4%;
Matches 457; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                their complementary sequences.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
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                                                1611 TTTATATTAGATACTAGTATGTGATTATTCCAAAT----ACATACTTTGGATGTTTAAA 1665
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Qy 뫄 γQ

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Db	Qy	DЪ	QУ	Db	Qy	DЬ	Qy	Db	Qy	DЪ	VΩ	Ф	Qy	DЬ	Qy
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Search completed: June 10, 2003, Job time: 737.005 secs 22:22:47

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/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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         sequence
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1, Appli

36, Appli

4, Appli

3, Appli

1, Appli

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535, Appli

535, Appli

124, Appli
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288, Appl
13, Appl
186, Appl
1137, Ap
651, App
 3, Appli
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651, App
27, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence 13, Application US/08487826B
Patent No. 5993827
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
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29 57.4 1.8 3095 6 5231168 1 30 56.6 1.8 168575 4 US-09-426-290.1 31 56.4 1.8 2058 2 US-08-949-391-1 32 56.4 1.8 2058 3 US-09-390-200-1 33 56.4 1.8 4673 1 US-07-638-431-1 34 56.4 1.8 4673 5 PCT-US92-00-1 35 56.2 1.8 1431 4 US-09-316-083-2 36 56.2 1.8 2960 3 US-08-913-842-3 37 55.6 1.7 701 4 US-08-913-842-3 38 55.6 1.7 5852 1 US-07-898-116-701 38 55.2 1.7 1406 3 US-08-913-842-6 40 55.2 1.7 1511 1 US-08-917-9578-8 41 55.2 1.7 1511 1 US-08-107-7558-8 42 55.2 1.7 1511 2 US-08-93-70-8618-8 43 55.2 1.7 1511 2 US-08-970-7558-8 44 55.2 1.7 1511 2 US-08-970-8618-8 45 55 1.7 1850 3 US-08-605-106-4	^	0					^			^	0			^	^			_
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	US-08-605-106-4	-617	US-09-370-861A-8	US-08-544-332-8	US-08-107-755A-8	US-07-991-867B-8	US-08-913-842-6	US-07-867-106-2	US-08-998-416-701	US-08-913-842-3	US-09-316-083-2	PCT-US92-00018-1	US-07-638-431-1	US-09-390-200-1	US-08-749-391-1	US-09-426-290-1	5231168-1	00 00 00 00 00 00 00 00 00 00 00 00 00

ALIGNMENTS

Peterson, David S.

BINDING PROTEINS

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MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
US-08-487-826B-13
                                                                                                                                                                                                                       TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA: ease #1.0, Version
APPLICATION NUMBER: US/08/487,826B
FILLING DATE: 10-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: UNITEDECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
                                                                                                                                                                 LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Knobbe Martens C
STREET: 620 Newport Center
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 92660
                                                                                                                                                TOPOLOGY:
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O Newport Center Drive 16th Floor
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Score 77.4
Pred. No.
    77.4; DB 2;
No. 1.8e-06;
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                       Length 19124;
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Matches

590;

Conservative

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Mismatches 781;

Indels

14;

Gaps

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TATATATTAGTATATGTTATCAAAATATTATAATATGTAAATT---ATTAATAAAATATA 1294
                                                       TGAGTATTACATTTTAAATTAAAGACAAAAATTTTTTGAAAAATGTTATAATTTTCTAACAAT 1972
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                           TTTAGTTATAAATACATTATGAACCAATAATAGTTGGTGAATTCAAATATCTCCATTAAT
                                                                                                               CAATTTTTTCTGCAAATATTAAATTAGGAATTCAATGCTACTATCAATAGAAGAAACAGC
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US-08-998-416-288
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Patent No. 6239264
GENERAL INFORMATI
                                                                   TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                        SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
                                                                                             REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 24-DEC-19
                                                                                                                                                                                                APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Meigs, J. Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                      TELEPHONE: 919-541-8689
                                                                                                                                          NAME: Meigs, J. Timot REGISTRATION NUMBER:
                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
             STRANDEDNESS:
                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1535
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                                                                                                                                                                                                                                                                                                                                                                                      Research Triangle Park
: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pohlmann, Rainer
Steiner, Sabine
Mohr, Christine
                                                                                                                                                                                                                                                                                                                                                                                                     E: No. 6239264artis Corporation 3054 Cornwallis Road sesearch Triangle Park
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Knechtle, Philipp
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RESULT 3
US-08-487-826B-13/c
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Best Local Similarity
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                               APPLICANT: Wellens, TITLE OF INVENTION: BTITLE OF INVENTION: ANUMBER OF SEQUENCES:
    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
                                                                                                                                     CORRESPONDENCE ADDRESS
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ORIGINAL SOURCE:
                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                         ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
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Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
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BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE
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Pred. No. 4.6e-05;
0; Mismatches 279;
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HYPOTHETICAL: N
ANTI-SENSE: NO
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Query Match 2.18;
Best Local Similarity 42.38;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
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FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
                                                                                                                                                                                       6624 ATCATATTTATATATTCATATATATATAATTGATATAGATACATATTCTTTGTATTGTTG
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                                                                        AATACGATTTTACAGCGTCACTAGTTGAGATTACTAGCATAAAGCATAAAGGACCCGTTC 1076
                                    ATTATTATATTATATTATATTATTAATAAAAATGTTTTTATCATT---TGTTTTGTTG
AAGCTATTTATACAAAGTTACAAACTGAATATAGCTTGAAATCCTTTAGAAAATTTTGGA
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619) 235-0176
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AACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTT
                                                                 GACTTATTATTCAGTATTCTTATTTTATTTTTTATTTTCCTTATTAAGATTAAAATAA 5322
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                                                                                                                    US-08-998-416-186
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US-08-998-416-186
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                                                        Query Match
Best Local Similarity
Matches 216; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 186, Application US/08998416 Patent No. 6239264
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: CH 001
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Me19s, J. Timothy
REGISTRATION NUMBER: 38,24
REFERENCE/DOCKET NUMBER: P
                                                                                                                                                                                                                                                   TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO:
                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                            TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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APPLICANT:
                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
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CITY: F
                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/998,416 FILING DATE: 24-DEC-1997
                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                  ORGANISM:
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Research Triangle Park
No. 6239264th Carolina
                  TGCATGGTGCGATTCAGAATT 2348
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VENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
                                                           Conservative
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Steiner, Sabine
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Knechtle, Philipp
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                                                                     2.1%;
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                                                                                                                                                                                                                                                                                                   38,241
ER: PF/5-30306/A/CGC1976
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                                                        Score 65.8; DB 4;
Pred. No. 0.00015;
0; Mismatches 227;
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                                                                                     Length 615;
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RESULT 5
US-08-998-416-1137
; Sequence 1137, Appl
; Patent No. 6239264
; Patent No. 6239264
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                                      TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
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                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                          TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: GENOMIC DNA SEQUITITLE OF INVENTION: AND USES THEREOF NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/998,416 FILING DATE: 24-DEC-1997 CLASSIFICATION: 435
                                                                                                                                                                                         REGISTRATIÓN NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTATAATGTATTTCCTATGTTCTTAAAATATTTTT----TTTTATATTTAGTTATAAAT 2045
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esearch Triangle Park
No. 6239264th Carolina
                                 636 base pairs
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Knechtle, Philipp
Rebischung, Corinne
Rebischung, Corinne
VENTION: GENOMIC DNA SEQUENCES
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Steiner, Sabine
Mohr, Christine
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US-09-641-638-651
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US-08-998-416-1137
                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6432648 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 651,
                                                                  CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
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Best Local
                                                                                                                                                                                                                          TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENEST.051CP1
                PRIOR FILLING L.... US UPRIOR APPLICATION NUMBER: US UPPRIOR A
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TOPOLOGY: line
MOLECULE TYPE: L
ORIGINAL SOURCE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2380 AACTTTAAAATAAATAAAATTTGAGTAAAT 2410
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Similarity 47.1%;
69; Conservative
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Chumakov, Ilya
Cohen, Annick
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Pred. No. 0.00018;
0; Mismatches 296;
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OTHER INFORMATION:
NAME/KEY: allele
LOCATION: 1827
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OTHER INFORMATION: 1
NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION: 1
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NUMBER OF SEQ ID NOS:
SOFTWARE: Patent.pm
OTHER INFORMATION: 10-510-173
NAME/KEY: allele
LOCATION: 2048
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LOCATION: 17555 .20674
OTHER INFORMATION: 3'regulatory region
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LOCATION: 16775..16945
OTHER INFORMATION: exon
NAME/KEY: exon
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LOCATION: 6349..6509
OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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LOCATION: 5552..5633
OTHER INFORMATION: exon
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OCATION: 1128
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OTHER INFORMATION: exon
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OCATION: 16567..16667
DTHER INFORMATION: exon
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LOCATION: 13308..13429
THER INFORMATION: exon
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LOCATION: 3871
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NAME/KEY: misc_feature
LOCATION: 1123..3123
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OCATION: 12854..13023
OTHER INFORMATION: exon
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OCATION: 8645
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OCATION: 7379
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OCATION: 3124..3297
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OCATION: 5758
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OTHER INFORMATION: 1
NAME/KEY: allele
LOCATION: 6338
OTHER INFORMATION: 1
NAME/KEY: allele
LOCATION: 6375
OTHER INFORMATION: 1
NAME/KEY: allele
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LOCATION: 6611
OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: allele
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LOCATION: 6534
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OTHER INFORMATION:
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LOCATION: 6141
OTHER INFORMATION:
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LOCATION: 4088
OTHER INFORMATION:
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LOCATION: 3802
OTHER INFORMATION:
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LOCATION:
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LOCATION: 2341
OTHER INFORMATION:
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NAME/KEY: allele
LOCATION: 2323
             NAME/KEY: allele LOCATION: 7668
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LOCATION: 6183
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OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: allele
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LOCATION: 4062
OTHER INFORMATION:
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LOCATION: 5903
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LOCATION: 2623
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INFORMATION: 10-348-391
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NAME/KEY: allele
LOCATION: 13535
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OTHER INFORMATION: 10-349-368
NAME/KEY: allele
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LOCATION: 13524
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OTHER INFORMATION:
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LOCATION: 8785
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LOCATION: 8777
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                        AGCAAATTTAAAAAATTATATAAGCC
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Pred. No. 0.0004;
0; Mismatches 206;
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RESULT 7
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Best Local Similarity 46.8%;
Matches 278; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08
FILING DATE: 06-Jul-1995
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Relaction DATA:
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DEDNESS: single
DGY: linear
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TATTAATATTTCCAATTAATATGAATACAATTATTAATATTTTGATGTGCACACATTA
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00 No. 5849573th Glebe
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    Mismatches

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Pred. No. 0.00074;
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; TYPE: DNA
; ORGANIZM: Plasmodium falciparum
US-09-150-741-1
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US-09-150-741-1
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CURRENT FILING DATE: 1998-09-10.
EARLIER APPLICATION NUMBER: PL6380
EARLIER FILING DATE: 1992-12-16
EARLIER APPLICATION NUMBER: AU93/00617
EARLIER FILING DATE: 1993-12-02
EARLIER APPLICATION NUMBER: 08/446,855
EARLIER FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 15
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Best Local Similarity 46.8%;
Matches 278; Conservative
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TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
Patent No. 6183996
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Pred. No. 0.00074;
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                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: 3871..4072
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 5552..5633
OTHER INFORMATION: exon 3
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CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
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TYPE: DNA
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OTHER INFORMATION: exon NAME/KEY: exon
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LOCATION: 7379..7522
OTHER INFORMATION: exon
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LOCATION: 6349..6509
OTHER INFORMATION: exon
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LOCATION: 5758..5880
OTHER INFORMATION: exon
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LOCATION: 3124..3297
OTHER INFORMATION: exon
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LOCATION: 1123..3123
OTHER INFORMATION: 5'regulatory region
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                                                                                   NAME/KEY: exon
LOCATION: 8645
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LOCATION: 5996
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Chumakov, Ilya
Cohen, Annick
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LOCATION: 2040
LOCATION: 1000
OTHER INFORMATION: 1
NAME/KEY: allele
NAME/KEY: 2323
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LOCATION: 2934
OTHER INFORMATION: 1
NAME/KEY: allele
LOCATION: 2947
INFORMATION: 1...
OTHER INFORMATION: 1
                                           LOCATION: 4109
OTHER INFORMATION:
NAME/KEY: allele
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OTHER INFORMATION: 10-512-318
NAME/KEY: allele
LOCATION: 2832
OTHER INFORMATION: 10-513-250
                                                                                             LOCATION: 4088
OTHER INFORMATION:
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NAME/KEY: allele
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LOCATION: 2623
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LOCATION: 2341
OTHER INFORMATION: 10-512-36
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LOCATION: 1827
OTHER INFORMATION:
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OTHER INFORMATION: 10-508-191
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OTHER INFORMATION:
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LOCATION: 3802
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OTHER INFORMATION: 10-513-365
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OTHER INFORMATION:
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LOCATION: 2844
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OTHER INFORMATION: 10-511-337
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LOCATION: 1182
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LOCATION: 17555..20674
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OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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LOCATION: 1559
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DTHER INFORMATION: 3'regulatory region
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NAME/KEY: allele LOCATION: 8777
OTHER INFORMATION: 10-349-216
NAME/KEY: allele LOCATION: 8785
OTHER INFORMATION: 10-349-224
                                                                    LOCATION: 13341
OTHER INFORMATION:
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                      NAME/KEY: allele LOCATION: 8658 OTHER INFORMATION:
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LOCATION: 7668
OTHER INFORMATION: 10-348-391
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OTHER INFORMATION:
NAME/KEY: allele
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OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: allele
                       NAME/KEY: allele LOCATION: 13524
                                           LOCATION: 13492
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 8926
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OTHER INFORMATION:
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Matches 224; Conserv

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Score 63; DB of Pred. No. 0.000 0; Mismatches

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Length 20674;

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US-08-817-926-27; Sequence 27, A
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APPLICANT: Komeda, Toshihiro
APPLICANT: Suda, Hisako
APPLICANT: Tamai, Yukio
APPLICANT: Tamai, Yukio
APPLICANT: Iwamatsu, Akihiro
APPLICANT: Iwamatsu, Akihiro
APPLICANT: Skato, No. 6001590uo
APPLICANT: Skato, Yasuyoshi
TITLE OF INVENTION: FORMATE DEHYDROGENASE GENE
                                                                                               APPLICATION NUMBER: US/08/817,926
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/02597
FILING DATE: 12-SEP-1996
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                   FILING DATE: 12-SEP-1995 PRIOR APPLICATION DATA:
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                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                          COUNTRY:
                      APPLICATION NUMBER:
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 27
SEQUENCE CHARACTERISTICS:
LENGTH: 4818 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local
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ORIGINAL SOURCE:
ORGANISM: Can
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                                                ATAGTTGGTGAATTCAAATATCTCCATTAATATTTTTTGAAATCTACAAATTATTAATAT 2121
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                                                                                                              TTATTATCGAAAAAACCTTAAAAAGGACTTCGTAAATTTTATTGTAATAAACGCAAAAA
                                                                                                                                           TTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAAATTTTGTTAACAGAAACTTCCAAA 2181
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(202)672-5399
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Pred. No. 0.001;
0; Mismatches 419;
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US-07-867-106-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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APPLICANT:
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TELEPHONE: 215-568-3439
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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FILING DATE: 19920625
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OPERATING SYSTEM: PC-DOS/MS-DOS
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        1947 TGAAAAATGTTATAATTTCTAACAATATTATTAAAATATGATGCCTATAATGTATTTCCT
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                                                                                                   ATGACAGCCTCTACAACTGTGATAGTCAATTTTTTCTGCAAATATTAAATTAAGGAATTCA 1886
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One Liberty Place 46th Floor
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Williams, Keith L
WENTION: Improved Plasmid Vectors for Cellular
WENTION: Slime Moulds of the Genus Dictyosteli
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Pred. No. 0.0015;
""smatches 217;
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US-09-316-083-2
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US-09-316-083-2
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Best Local Similarity
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APPLICANT: The Institute of Physical and Chemical Research
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 215;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/316,083A CURRENT FILING DATE: 1999-05-20 EARLIER APPLICATION NUMBER: JP98/141861 EARLIER FILING DATE: 1998-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Endonuclease FILE REFERENCE: PH-651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Saccharomyces
FEATURE:
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2258- AGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTCAAAGTATGTTATCTAGTAGGTG
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                                                                          AACAAGAATAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTA 225
                                                                                                                                       AATTATTATATACTTATTTTATATTTTAAATAAAATGAAAATGGAAATGGATAATTATA
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                                               ATAAATATTTAATTAATAAATATATGAAATATTTAGATATGTTAAATATGATTCCTAATA
                                                                                                         ATATCTCCATTAATATTTTTTGAAATCTACA-AATTATTAATATTTAGTCAATAACAATG 2137
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Pred. No. 0.0014;
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US-08-817-926-27/c
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                                                                                                   Query Match
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 0813
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: don't'
TOPOLOGY
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 12-SEP-1995
PRIOR APPLICATION DATA:
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APPLICANT: Sakai, Yasuyoshi
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TITLE OF INVENTION: FORMATE DEHYDROGENASE GENE
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                                                                     Local Si
hes 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/
FILING DATE: 12-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 42536/1996 FILING DATE: 29-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                 54 TICTGGTTATTCTGTTCACATGATTTGAGTTTGGGTTCTCAAGTTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTAGTT 113
                                                                                 similarity 46.3%;
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TAAATAATAATGAATTTATGATTATTATCAGG 617
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                        (202)672-5399
                                                                     Conservative
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Kato, No. 6001590uo
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                                                                                                                                                    Candida boidinii
                                                                                                                                                                                 DNA (genomic)
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                                                                  0;
                                                                                 Score 60.8; DB 3
Pred. No. 0.0023;
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                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.30
                                                                                               DB 3;
                                                                  312;
                                                                                               Length 4818;
                                                                Indels
                                                                  7;
                                                                  Gaps
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US-08-998-416-288/c
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                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
ATTORNEY/AGENT INFORMATION:
               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 01
FILING DATE: 31-DEC-1996
                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rebischu
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                             COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                APPLICATION NUMBER: FILING DATE: 24-DE
                                                                                                                                                                                                                                                  ADDRESSEE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                  COUNTRY:
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3. 6239264
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Knechtle, Philipp
                                                                                                                                                                                                                                      USA
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/ENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mohr, Christine
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Steiner, Sabine
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                                                                                24-DEC-1997
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1152
                                 CH 0016/97
                                                                                                 US/08/998,416
                                                                                                                                  Version #1.30
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                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08446855A Patent No. 5849573
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                APPLICANT: Stewart, Thomas S
APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
NUMBER OF SEQUENCES: 2
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ORIGINAL SOURCE:
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LENGTH: 837 base pairs
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TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                COUNTRY: USA
ZIP: 22201-4714
                                                                                                                                             STREET: 1100 NO CITY: Arlington
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TOPOLOGY: lir
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               SOFTWARE:
                                                                                                                                   STATE: Virginia
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                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                    1100 No.
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nilarity 49.1%;
Conservative
                 PatentIn Release #1.24
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                                                                                                                                                                 Nixon & Vanderhye PC
00 No. 5849573th Glebe Road,
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Pred. No. 0.0017;
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                                                                                                                                                                  8th Floor
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8920 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/446
FILING DATE: 06-Jul-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.09
REFERENCE/DOCKET NUMBER: 47-8
                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 703-816-4000
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Local Similarity 48.8%;
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8451
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                            2219 AACTATTTTGTTGGAATGGAAGTAGTAATATA 2252
                                                                                                                                                                                                                                                       nucleic acid
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                                                                                   TTTTGTTAACAGAAACTTCCAAATTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAA 2218
                                                                                                                                                                       TATAAAAAATAAATCAATATAAATTAATGATCATATTTAATAAAAACATTTATTAATAT
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Search completed: June 11, Job time: 155.509 secs 2003, 01:53:50

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Title:
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Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                       : /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq: *
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq: *
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq: *
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq: *
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/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq: *
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq: *
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/cgn2_6/ptodata/1/pubpna/US00_PUBCOMB.seq: *
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                                                                                                                                                                                               /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
SUMMARIES
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No.	Score	Match	Query Match Length DB	DB	ID	Description
c 1	91.6	2.9	960	9	US-10-198-846-6381	Sequence 6381, Ap
ი 2	82.6	2.6	15732	9	US-10-239-676-95	Sequence 95, Appl
C S	81.6	2.5	5689	9	US-10-239-676-90	Sequence 90, Appl
4	80	2.5	640681	10	US-09-790-988-1	Sequence 1, Appl:
տ	79.4	2.5	960	9	US-10-198-846-6381	Sequence 6381, Ap
თ	75.2	. 2.3	5979	9	US-10-239-676-18	Sequence 18, Appl
7	73.4	2.3	5689	9	US-10-239-676-90	Sequence 90, Appl
о С	73	2.3	5979	œ	US-10-239-676-18	Sequence 18, Appl
9	71.2	2.2	15732	9	US-10-239-676-96	Sequence 96, Appl
10	71	2.2	12405	9	US-10-239-676-35	Sequence 35, Appl
c 11	68.8	2.1	335913	9	US-09-754-853A-2	Sequence 2, Appli
c 12	68.8	2.1	335913	Q	US-09-754-853A-3	Sequence 3, Appli
c 13	68	2.1	6298	9	US-10-239-676-64	Sequence 64, Appl
c 14	89	$^{2.1}$	11260	9	US-10-239-676-20	Sequence 20, Appl
c 15	67.4	2.1	5917	9	US-10-087-464-9	Sequence 9, Appli
c 16	67.2	2.1	4985	9	US-10-094-240-10	Sequence 10, Appl
c 17	67.2	2.1	8588	9	US-10-239-676-178	
18	67	2.1	4985	9	US-10-094-240-10	Sequence 10, Appl
c 19	66.6	2.1	640681	10	me-00-700-088-1	Sequence 1. Appl

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Sequence 209, App Sequence 1, Appli		Sequence 202, Appl Sequence 96, Appl Sequence 24, Appl	210,	196,	28,	159	Sequence 11254, A	Sequence 1212, Ap	Sequence 195, App	Sequence 46, Appl	Sequence 3, Appli	Sequence 2, Appli	Sequence 210, App	Sequence 30, Appl	Sequence bu, Appl			N.

ALIGNMENTS

/c / C	; FEATURE: ; NAME/KEY: ; LOCATION: ; LOCATION:	OTHER INE FEATURE: NAME/KEY: LOCATION: LOCATION: LOCATION: LOCATION: COTHER INE	SOFTWARE: SOFTWARE: SEQ ID NO 6 LENGTH: 9 LENGTH: 9 LENGTH: DNA ORGANISM: ORGANISM: ORGANISM: LOCATION: LOCATION: LOCATION: LOCATION:	RESULT 1 (S-10-198-846-6381, A) Sequence 6381, A) PUDLICANT: Lill APPLICANT: Lill APPLICANT: Wan APPLICANT: Wan APPLICANT: Ste TITLE OF INVENT TITLE APPLICA CURRENT APPLICA CURRENT FILING CURRENT F
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AND METH PREVENTI 7, 119, 1: 30, 249, 330, 249, 330, 249, 351, 299, 122, 424, 359, 575, 559, 575, 559, 67	• •			6 POSITION ASS T CANCE 8,846
PREVENTI 119, 1: 0, 249, 1, 299, 1, 299, 575, 9, 575, 9, 575, 9, 6778,	840, 900,	487, 555, 658, 748,	88, 13 194, 286, 411,	R RITS,
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AND 134. 0, 253, 7, 333, 7, 516, 8, 588, 6, 686, 9, 861, 4, 907,	849, 86 904, 90	513, 580, 685, 802	72,0	**

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357; Conservative
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                                                                                                                                      CATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTCAAAGTATGTTATCTAGT
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                                                                                                           ANTTATTNANTTTTAAAAAAAAAAAAAAAAAAAAAACCGNGNNNGGNCNAGAGTACNTGCC
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-239-676-95
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2000-09-01
NUMBER OF SEQ ID N
SEQ ID NO 95
LENGTH: 15732
TYPE: DNA
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Hest Local Similarity 43.9%;
Matches 453; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
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2000-04-06
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CURRENT FILING DATE: 2002-09-24
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TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 5013.1003
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GACAAAATTTTTGAAAAATGTTATAATTTCTAACAATATTATTAAAATATGATGCCTATA 1995
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                                                             AAAAAAACTTTTTAAAAAAAATAATATAACTTAAAATAAACTTAAATCAATAAATATCAA
                                                                                        GAATTCAATGCT----ACTATCAATAGAAGAAACAGCTGAGTATTACATTTTAATTTAAA
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Pred. No. 0.0005;
D; Mismatches 574;
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; LOCATION: (1818, 1930..1931, 1934..1935,
US-10-239-676-90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 90, Application US/10239676 Publication No. US20030082609A1 GENERAL INFORMATION:
                            Query Match
Best Local Similarity
Matches 285; Conserv
                                                                                                                                                                                                    SEQ ID NO 90
LENGTH: 5689
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 10032529.7
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
                                                                                                                                                                                                                                 2000-09-01
NUMBER OF SEQ
                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 5013.1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: OLEK, Alexander
                                                                                                                               FEATURE: OTHER INFORMATION: chemically treated genomic DNA FEATURE:
                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                        TYPE: DNA
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                           Score 81.6; DB 9;
Pred. No. 0.00049;
0; Mismatches 292;
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Best Local
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                                          324686 ATATTGTTAGTATTCTTTTTTATATTACCAATATATTTATCATCAATTAATATTGGCAAC 324745
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                                                                       1559 ATATTTATTGTTAGTTGGAATTTAATAAGAGCGAACTTGTAACATTTACAATATTTATATT
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; ORGANISM: Buchnera US-09-790-988-1
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                                                                                                                                                                                                                                                          APPLICANT: WATANABE, HIDEMI APPLICANT: HATTORI, MASAHIRA APPLICANT: SAKAKI, YOSHIYUKI TITLE OF INVENTION: GENOME DNA FILE REFERENCE: 081356/0159
                                                                                                                                                        NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/790,988 CURRENT FILING DATE: 2001-02-23 PRIOR APPLICATION NUMBER: JP2000-107160 PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                      APPLICANT: SHIGENOBU, SHUJI APPLICANT: WATANABE, HIDEM
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                Similarity
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Conservative
              2.5%;
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                Score 80; DB 10;
Pred. No. 0.0057;
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Mismatches 455;
                                 DB 10;
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                                 Length 640681;
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APPLICANT: Lilie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KI
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TIPLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
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US-10-198-846-6381
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                                                                                                                                                                                                                                 Sequence 6381, Application US/10198846 Publication No. US20030099974A1
   NUMBER OF
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                                                                                                                ASSESSMENT,
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SEQ ID NO 6381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 40.9
Matches 312; Conservative
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Best Local
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NAME/KEY: misc_feature
LOCATION: 807, 808, 819, 820, 821,
LOCATION: 871, 874, 875, 891, 892,
LOCATION: 917, 923, 925, 926, 927,
LOCATION: 917, 923, 925, 926, 927,
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LOCATION: 428, 433, 450, 465,
LOCATION: 517, 518, 528, 530, 534,
LOCATION: 590, 610, 625, 626, 642,
LOCATION: 690, 700, 702, 706, 716,
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE: MAME/KEY: misc_feature  
LOCATION: 1, 8, 66, 71, 79, 81, 84, 85, LOCATION: 149, 156, 162, 166, 172, 179, LOCATION: 268, 271, 273, 274, 275, 276, LOCATION: 359, 366, 374, 393, 404, 406, OTHER INFORMATION: n = A,T,C or G
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          CAATAACAATGCATAGAAAGTTCCAAAAAAAATTTTGTTAACAGAAACTTCCAAATTTTT 2186
                                            TGAAAAATGTTATAATTTCTAACAATATTATTAAAATATGATGCCTATAATGTATTTCCT
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                                                                                                                                             ATGTTCTTAAAATATTTTTTTTTATATTTAGTTATAAATACATTATGAACCAATAATAGT 2066
                                                                                                                                                                              AAAAAATTAATTTTTTAATNTNNAANNNAAAAAATTNTNTTTTNAATTNAAGGTTTTTAA
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Pred. No. 0.00057;
0; Mismatches 445;
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895, 898,
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; 2000-09-01
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 18
; LENCTH: 5979
; TYPE: DNA
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: chemically treated genomic DNA US-10-239-676-18
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US-10-239-676-18
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Best Local Similarity
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APPLICANT: OLEK, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18, Application US/10239676 Publication No. US20030082609A1
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TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
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     GAGTATTACATTTAAATTTAAAGACAAAATTTTTGAAAAATGTTATAATTTCTAACAATA 1973
                                                                                                            AATTTTTTCTGCAAATATTAAATTAGGAATTCAATGCTACTATCAATAGAAGAAACAGCT
                                                                                                                                                 ATATATATTTAATATTTTTTTATATTTTAAATTAAGTAAGTATATATTTATTTTAATA
                                                                                                                                                                                 ATAGATTAATTACCGTATGTTTTTGTTGCCATAATGACAGCCTCTACAACTGTGATAGTC 1853
                                                                                                                                                                                                                     TAAATACGATTATTTTAAATTAGTAATTTAAGAAATTTTACGTTTAAATTTAATAGAAA 1698
                                                                                                                                                                                                                                                       GCGATGCATGAAGGATAAACCTAATGACTTTAATTTTTTGAAAATGTAACCCTTTTACTC 1793
                                                                                                                                                                                                                                                                                          TTATAATTATAATATTTATTTTTTATATTGATTTAGGTAAAAATTTAAGAGTATGGTT 1638
                                                                                                                                                                                                                                                                                                                            TGTTTCTTCCTACGGTATAATATTAATCATCGAGGTAAAAAAGTTTTGTCTTATTTTC 1733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 75.2; DB 9; Pred. No. 0.0056;
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                                                                                                            ; NAME/KEY: unsure
; LOCATION: (1818, 1930..1931, 1934..1935, 1947..1948,
US-10-239-676-90
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US-10-239-676-90
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                                     Query Match
Best Local Similarity
Matches 304; Conserv
                                                                                                                                                                                                               SEQ ID NO 90
LENGTH: 5689
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 90, Application US/10239676 Publication No. US20030082609A1
                                                                                                                                                                                                                                                                                                                                                            DE 10043826.1
PRIOR FILING DATE: 2001-04-06
2000-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
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                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: OLEK,
                                                                                                                                                                    FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                  FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                DE 10019058.8
DE 10019173.8
DE 10032529.7
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TTATTA--AAATATGATGCCTATAAATGTATTTCCTATGTTTCTTAAAATATTTTTTTAT
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                                                      2.3%;
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                                 Score 73.4; DI
Pred. No. 0.011
0; Mismatches
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                                                                   DB 9;
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2000-09-01
NUMBER OF SEQ ID N
SEQ ID NO 18
LENGTH: 5979
                                                                                                                                                                                       Sequence 18, Application US/10239676
Publication No. US20030082609A1
GEMERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPEMBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases
FILE REFERENCE: 5013.1003
                                               PRIOR FILING DATE: ; 2000-04-06 2000-04-07 2000-06-30
                                                                                                 CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILLING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 1003529.7
DE 10043826.1
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US-10-239-676-18
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Best Local Similarity 45.1%;
Matches 482; Conservative
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ORGANISM: Artificial Sequence
FEATURE:
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TTACTACGAAATTTATCTTTATATATAAAATATAAAATTAAAACAATTTAAAATTATAAAT
                      GTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTAT 2287
                                               TTACATAAAAAAATAATTCAAATTAATTATTTTATATTAATCATACTATTTATA
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Pred. No. 0.013;
0; Mismatches 570; Indels
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US-10-239-676-96
; Sequence 96, Application US/10239676
; Publication No. US20030082609A1
; GENERAL INFORMATION:
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US-10-239-676-96
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2000-06-30
2000-09-01
NUMBER OF SEQ ID N
SEQ ID NO 96
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Best Local Similarity 42.8%;
Matches 968; Conservative
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APPLICANT: PIEPEMBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene
FILE REFERENCE: 5013.1003
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 15732
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                          TAGATCTTTTGGGTTACAGTTTCGAAGTCCTCTACAAGCGTGTAACCATCTGCAACTATT
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RESULT 10
US-10-239-676-35
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Publication No. US20030082609A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases
FILE REFERENCE: 5013.1003
                                                                                            CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILLMG DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 1003529.7
DE 10043825.1
                                                                                 PRIOR FILING DATE:
                                 2000-04-07 2000-06-30
                                                               2000-04-06
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RESULT 11
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NUMBER OF SEQ ID NOS:
SEQ ID NO 35
LENGTH: 12405
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Best Local Similarity
Matches 347; Conserv
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                                                                                                                                       GTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATA
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nilarity 45.0%;
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Pred. No. 0.036;
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; LOCATION: (45163)..(45314),(45450)..(45509),(46941)..(48763),(48975)..(49573)
; OTHER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853A-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Publication No. US20030005491A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated TITLE OF INVENTION: Soybean Cyst Nematode Resistance FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR EILING DATE: 2000-01-07
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TYPE: DNA
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Parsons, Jeremy D.
TAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTT 2266
                                                                                                                   AATATTTTTTGAAATCTACAAAT---TATTAATATTTTAGTCAATAACAATGCATAGAAAG 2146
                                                                                                                                                                                               ATATTTAGTTATAAATACATTATGAACCAATAATAGTTGGTGAATTCAAATATCTCCATT
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Pred. No. 0
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; FEATURE:
, NAME/KEY: CDS
, LOCATION: (46798)..(48763),(48975)..(49573)
, OTHER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853A-3
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Best Local S
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SEQ ID NO 3
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TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Scybean Cyst Nematode
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
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              AGCTGAGTATTACATTTTAAATTTAAAGACAAAATTTTTGAAAAATGTTATAATTTCTAAC
                                                AATTTCTTCATACAAAATAATAATATTATTTCATAAATTATAAGTTTAATATTAGCTAC
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                                                                                   AGTCAATTTTTTCTGCAAATATTAAATTAGGAATTCAATGCTACTATCAATAGAAGAAAC
                                                                                                                     ACTCATAGATTAATTACCGTATGTTTTTGTTGCCATAATGACAGCCTCTACAACTGTGAT 1849
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Resistance
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                                                                                                     ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-239-676-64
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NUMBER OF SEQ ID N
SEQ ID NO 64
LENGTH: 6298
                                                 Query Match
Best Local S
Matches 273
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DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
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CURRENT FILING DATE: 2002-09-24
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TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
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                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OLEK, Alexander
                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-04-06
                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                       TYPE: DNA
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2000-04-07
2000-06-30
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1850 AGTCAATTTTTTCTGCAAATATTAAATTAGGAATTCAATGCTACTATCAATAGAAGAAAC 1909
                                                              Similarity
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                                                  Conservative
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                                                             2.1%;
                                               Score 68; DB 9;
Pred. No. 0.087;
0; Mismatches 28
                                                  280;
                                                                       Length 6298;
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         Query Match
Best Local Similarity
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                                                                                                                          SEQ ID NO 20
LENGTH: 11260
                                                                                                                                                   2000-09-01
NUMBER OF SEQ
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PRIOR FILING DATE:
                                                                                     FEATURE:
                                                                                                               TYPE: DNA
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           Conservative
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-239-676-20
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DE 10019058.8
DE 10019173.8
DE 10032529.7
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CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
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TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
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                                                                                                                                         ORGANISM: Artificial Sequence
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                       2.18;
Score 68; DB 9;
Pred. No. 0.11;
0; Mismatches 29
                                          Length 11260;
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295;

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; ORGANISM: Plasmodium falciparum
US-10-087-464-9
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US-10-087-464-9/c
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                                                                  Query Match
Best Local Similarity
Matches 211; Conserv
                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 06/272,930
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 5917
                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Chishti, Athar
APPLICANT: Oh, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/10087464 Publication No. US20030059436A1
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                              APPLICANT: Li, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
FILE REFERENCE: S1237/7019
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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1848 ATAGTCAATTTTTTCTGCAAATATTAAATTAGGAATTCAATGCTACTATCAATAGAAGAA 1907
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Liu, David
Goel, Vikas
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Search completed: June 11, 2003, 08:07:41 Job time: 463.588 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	125	3.9	826		PCT-US99-22853B-3486	
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c 15	91.6	2.9	960	41	US-10-198-846-6381	
	91.6	2.9	464387	ယ္သ	US-09-948-941-643	_
17	89.2	2.8	98573	68	US-60-248-505-542	
18	88.4	2.8	1368	38	US-10-015-127-2421	
c 19	87.6	2.7	908	56	US-60-126-265-3038	
c 20	87.6	2.7	27978	64	US-60-207-423-22	
c 21	87.6	2.7	32768	64	US-60-207-423-23	

Qy 121 AAAATTCATTTAAAATATTTACAAGTAATTATCTTTACATTGTTATTATAACAA 180	atches 3202; Conservative 0; Mismatc 1 ATGTGGGTATTATATTGTTGGGTTCGGTTT	H: 6888 DNA ISM: Arabidopsis sp. 03820-1 atch	CURRENT FILING DATE: 2000-02-11 EARLIER APPLICATION NUMBER: 60/119,657 EARLIER FILING DATE: 1999-02-11 EARLIER APPLICATION NUMBER: 60/119,658 EARLIER FILING DATE: 1999-02-11 NUMBER OF SEO ID NOS: 18 SOFTWARE: PATENTIN Ver. 2.0 SEO ID NO 1	PCT-US00-03820-1 PCT-US00-03820-1 ; Sequence 1, Application PC/TUS0003820 ; GENERAL INFORMATION: ; APPLICANT: THE ARIZONA BOARD OF REGENTS ON BEHALF OF THE UNIVERSITY OF ARIZONA. ; TITLE OF INVENTION: DWF4 POLYNUCLECTIDES, POLYPEPTIDES AND USES THEREOF ; FILE REFERENCE: 2225-0001.40 ; CURRENT APPLICATION NUMBER: PCT/US00/03820		86.8 2.7 755 38 186.6 2.7 720 18 18 18 18 18 18 18 18 18 18 18 18 18	35 87 2.7 868 27 US-09-684-016-367906 Sequence 36 87 2.7 868 64 US-60-207-458-32398 Sequence 37 87 2.7 1368 38 US-10-015-127-2421 Sequence 38 87 2.7 1368 38 US-10-048-823-33 Sequence 39 86.8 2.7 755 24 US-60-634-306B-128109 Sequence	30 87.4 2.7 32768 65 US-60-213-181-33 Sequence 31 87.4 2.7 32768 65 US-60-213-181-34 Sequence 32 87.4 2.7 32768 65 US-60-213-181-35 Sequence 33 87.4 2.7 158001 42 US-10-211-179-11 GENERAL 34 87 2.7 868 25 US-09-654-617-367906 Sequence	2.7 32768 64 US-60-207-905-22 Sequenc 2.7 32768 64 US-60-207-905-23 Sequenc 2.7 32768 64 US-60-207-905-24 Sequenc 2.7 32768 64 US-60-208-837-26 Sequenc 2.7 32768 64 US-60-208-837-27 Sequenc 2.7 32768 64 US-60-208-837-27 Sequenc 2.7 32768 64 US-60-207-458-34124 Sequenc 2.7 32768 65 US-60-212-657-88 Sequenc
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      Sequence 1, Application US/09502426
GENERAL INFORMATION:
APPLICANT: AZPIROZ, Ricardo
APPLICANT: CHOE, Sunghwa
APPLICANT: FELDMANN, Kenneth
TITLE OF INVENTION: DWF4 POLYNUCLEOTIDES, PO:
FILE REFERENCE: 2225-0001
CURRENT APPLICATION NUMBER: US/09/502,426
CURRENT FILING DATE: 2000-02-11
EARLIER APPLICATION NUMBER: 60/119,657
EARLIER APPLICATION NUMBER: 60/119,657
EARLIER FILING DATE: 1999-02-11
EARLIER FILING DATE: 1999-02-11
EARLIER FILING DATE: 1999-02-11
SEARLIER FILING DATE: 1999-02-11
EARLIER FILING DATE: 1999-02-11
SEARLIER FILING DATE: 1999-02-11
LENGTH: 6888
TYPE: DNA
DEPARTER: ARCHIEVE TO NOS: 18
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof

FILE REFERENCE: 98-10(15493)C

CURRENT APPLICATION NUMBER: US/09/692,412

CURRENT FILING DATE: 2000-10-24

NUMBER OF SEQ ID NOS: 124

SEQ ID NO 94

LENGTH: 84196

TYPE: DNA

ORGANISM: Arabidopsis thaliana

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; Sequence 94, Application US/09692412
; GENERAL INFORMATION:
Bush, David F.
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Similarity 99.5%;
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APPLICANT: ALEXANDROV, Nickol
APPLICANT: CLEN, Xianfeng
APPLICANT: SUBRAMANIAN, Gopal
APPLICANT: ZHENG, Liansheng
TITLE OF INVENTION: SEQUENCE-
FILE REFERENCE: 2750-0662P
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                                                                 CURRENT APPLICATION NUMBER: US/09/451,320
CURRENT FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 6998
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2050
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                                       TYPE: DNA ORGANISM: Arabidopsis thaliana FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 94, Application US/09692412 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3486, Application PC/TUS9922853B GENERAL INFORMATION:
                                                                                                                                                                Matches 158;
                                                                                                                                                                                                                                                                          SEQ ID NO 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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SEQ ID NO 3486
                                                                                                                                                                             Best Local
                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 125;
                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 38-10(15493)C CURRENT APPLICATION NUMBER: US/09/692,412 CURRENT FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ceres, Inc.
TITLE OF INVENTION: Sequence-Determined DNA Fragments
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-0569F(PC)
CURRENT APPLICATION NUMBER: PCT/US99/22853B
CURRENT FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 3938
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bush, David F. APPLICANT: Rounsley, Steven D. APPLICANT: Wiegand, Roger C. TITLE OF INVENTION: Plant
                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                             LENGTH: 84196
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: UNSURE
LOCATION: (1).(826)
OTHER INFORMATION: any n = any nucleic acid, unknown or other
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TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: LOCATION 1..826, Ceres
                                                                                                         33161 TATAGAAATTCGTTAAAATTTGCGATAACGAGTGTCAAAAATATTTTATTTGTTAGCTGA
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                                                                                                                     763 TCTGGATATTCGTTAAAATTTGCGATAACGATTGTGAAAAATATTTTATTTGTTAGCTGA 822
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Similarity 83.2%;
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              CTTTTTGTTTCGTTTCCTCTTAACTATATTATCGCGGATATATGATAACAATGATATAT 941
CTTTTTGTTTCATTTCTCTTAACTTGATAATATTGCGGATATATGAAAAAACATGTCTTAG
                                                   TCTCAATATTATGTTCCAGGTATTTGCATAATCTTCTGTTTAAAGCATA-TTTTGTCTTT
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                                                                                                                                                              0; Mismatches
                                                                                                                                                                          Score 118; DB 27;
Pred. No. 3.7e-07;
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US-60-207-458-33653; Applied to the second s
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; ORGANISM: Arabidopsis thaliana
US-09-803-736-1074
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US-09-803-736-1074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1074, Application US/09803736 GENERAL INFORMATION:
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TITLE OF INVENTION:

TITLE OF INVENTION:
PLANTS
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/60/207,458
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS:
152403
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APPLICANT: Norris, Susan R.
APPLICANT: Rounsley, Steven D.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof FILE REFERENCE: 38-10 (15493)D
FULL REFERENCE: 38-10 (15493)D
CURRENT APPLICATION NUMBER: US/09/803,736
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 09/534,859
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
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La Rosa, Thomas J.
Lalgudi, Raghunath V.
                                                                                                                                                                                              Shukla, Hridayabhiranjan
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Pred. No. 3.7e-07;
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                                                                                                                                  AND OTHER MOLECULES ASSOCIATED WITH
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TYPE: DNA
ORGANISM: Zea 1
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  TTATATTATTTA 988
                                                                                     ATATAAATATTATTATTTATTTTAATATATATCATAAACTATATTTTATTCTTTAATTT
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49.3%;
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NAME/KEY: unsure

LOCATION: (1)...(1326)

OTHER INFORMATION: unsure at all n locations
US-09-663-779-8205
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Best Local Similarity
Matches 561; Conserv
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LENGTH: 1326
TYPE: DNA
ORGANISM: Bacillus thuringiensis
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CURRENT FILING DATE: 2000-09-15
PRIOR FILING DATE: 60/154,678
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 8700
PRIOR DIO 8205
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APPLICANT: Malvar, Thomas M.
APPLICANT: Shukla, Hridayabhiranjan
TITLE OF INVENTION: BACILLUS THURINGIENSIS
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 38-21(51376)B
 1811 TGTTTTTGTTGCCATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTTCTGCAAATA 1870
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                                  AGTTGGAATTTAATAAGAGCGAACTTGTAACATTACAATATTTATATTAGATACTAGTAT
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NAME/KEY: unsure
LOCATION: (1)...(1326)
OTHER INFORMATION: unsure at all n locations
US-09-663-779-8205
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    Query Match
Best Local S
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LENGTH: 1326
TYPE: DNA
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                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PRIOR FILING DATE: NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                               FILE REFERENCE: 38-21(51376)B
CURRENT APPLICATION NUMBER: US/09/663,779
CURRENT FILING DATE: 2000-09-15
                                                                                                                                                                                                                                                                             TITLE OF INVENTION: THEREOF FILE REFERENCE: 38-21(
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Shukla, Hridayabhiranjan
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    Conservative
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                3.1%;
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1999-09-17
                                                                                                                                                                                                                                                                                                            BACILLUS
Score 98.2; DB 26;
Pred. No. 0.00015;
D; Mismatches 503;
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                              Length 1326;
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APPLICANT: Fincher, Karen L. APPLICANT: La Rosa, Thomas J. APPLICANT: Xiao, Jinhua TITLE OF INVENTION: Nucleic Acid TITLE OF INVENTION: Plants
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              And
              Other
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             Associated
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(810)
; OTHER INFORMATION: unsure at
; OTHER INFORMATION: Clone ID:
US-09-666-355A-6400
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CURRENT APPLICATION NUMBER: US/09/666,3554
CURRENT FILLING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US 60/155,005
PRIOR FILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 25978
SEQ ID NO 6400
PLENGTH: 810
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Best Local
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                                   AATTTTTTTTTTTATGGAA 2199
                                                                                                                              TAATAGTTGGTGAATTCAAATATCTCCATTAATATTTTTTGAAATCTACAAATTATTAAT 2119
                                                                                                                                                                                                                AAATTTTTGAAAAATGTTATAATTTCTAACAATATTATTAAAATATGATGCCTATAATGT 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTAACAGAAACTTCCA 2179
                                                                                                                                                                            ATTTCCTATGTTCTTAAAATATTTTTTTTTTTATATTTAGTTATAAATACATTATGAACCAA 2059
                                                                                                                                                                                                   GAATTCAATGCTACTATCAATAGAAGAAACAGCTGAGTATTACATTTTAAATTTAAAGACA 1939
                                                                                                                                                                                                                                                                                                                  TGCCATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTCTGCAAATATTAAATTAG 1879
                                                                                                                                                                                                                                                                                                                                                              ATCATCGAGGTAAAAAAAGTTTTGTCTTATTTTCGCGATGCATGAAGGATAAACCTAATG 1759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTAATAAGAGCGAACTTGTAACATTACAATATTTATATTAGATACTAGTATGTGATTATT 1639
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45.5%;
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uC-gsronu33B029g09b1
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GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN
TITLE OF INVENTION: ACID MOLECULES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 630
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 22350
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 565;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/60/245,228 CURRENT FILING DATE: 2000-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
                                                                              4844
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TCAATGCTACTATCAATAGAAGAAACAGCTGAGTATTACATTTTAATTTAAAGACAAAAT 1943
                        ATTATTATATATATATATATATATATATATATATATT-ATTATATATATATATATATATATATATA
                                                                                                 ATACATACTTTGGATGTTTAAACTTAATCTTGTTTCTTCCTACGGTATAAATATTAATCA 1703
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                                                                                                                                                                                                                                                                               ATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTTCTGCAAATATTAAATTAGGAAT
                                                                                                                          TCGAGGTAAAAAAGTTTTGTCTTATTTTCGCGATGCATGAAGGATAAACCTAATGACTT
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; NUMBER OF SEQ ID NOS: 8283

; SEQ ID NO 3024

; LENGTH: 742

; TYPE: DNA

; ORGANISM: Bacillus thuringiensis

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US-09-663-779-3024/c
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Best Local Similarity
Matches 326; Conserv
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CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/154,678
PRIOR FILING DATE: 1990-00-17
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                1658 TGTTTAAACTTAATCTTGTTTCTTCCTACGGTATAAATATTAATCAT----CGAGGTAAA 1713
                                                                                                                                     1538
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                                                                           TTTCTTTAATGCATCTTTAACATATTTATTGTTAGTTGGAATTTAATAAGAGCGAACTTG 1597
ATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTGGGACAACAATG 2360
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Shukla, Hridayabhiranjan
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                                                                                                                                                               Conservative
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                                                                                                                                                                         3.0%;
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1999-09-17
                                                                                                                                                                                                                                                                                                                                                                            BACILLUS THURINGIENSIS CHROMOSOMAL GENOME SEQUENCES
                                                                                                                                                          Score 94.6; DB 26;
Pred. No. 0.00046;
0; Mismatches 344;
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APPLICANT: Wang, YOUZhen

APPLICANT: Steinmann, Kathleen

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS

TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: THERAPY OF BREAST CANCER

FILE REFERENCE: MRI-049

CURRENT APPLICATION NUMBER: US/10/198,846

CURRENT FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR APPLICATION NUMBER: 05/306,220

PRIOR APPLICATION NUMBER: 00/306,220

PRIOR FILING DATE: 2001-07-18

NUMBER OF SEG ID NOS: 14084

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6381
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US-10-198-846-6381/c
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                                                                                                                                          FEATURE:

NAME/KEY: misc_feature

LOCATION: 1, 8, 66, 71, 79, 81, 84, 85, 86

LOCATION: 149, 156, 162, 166, 172, 179, 18

LOCATION: 268, 271, 273, 274, 275, 276, 27

LOCATION: 359, 366, 374, 393, 404, 406, 46
FEATURE:

NAME/KEY: misc_feature

NAME/KEY: misc_feature

LOCATION: 428, 433, 450, 465, 466, 46

LOCATION: 517, 518, 528, 530, 534, 53

LOCATION: 590, 610, 625, 626, 642, 64

LOCATION: 690, 700, 702, 706, 716, 7:

COCATION: MEDICAL COLUMN TO ALTICOLORY TO GENERAL COLUMN TO THE ALTICOLORY TO THE ALTI
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APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzher
APPLICANT: Steinmann, Ke
                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                      OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                    LENGTH: 960
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NAME/KEY: misc_feature

; LOCATION: 807, 808, 819, 820, 821,

; LOCATION: 871, 874, 875, 891, 892,

; LOCATION: 917, 923, 925, 926, 927,

; OTHER INFORMATION: n = A,T,C or G

US-10-198-846-6381
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Best Local Similarity
Matches 357; Conserv
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                                                                                             CATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTCAAAGTATGTTATCTAGT
                                                                                                                                      TAAAAANNTTAAAANAATAGNATTNTTGAANTTAAATNTTTAAATATCTTTTNAATTAAA
                                                                                                                                                                           TATGGAACAAGAAATAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATA 2252
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ilarity 39.5%;
Conservative
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Pred. No. 0.0013;
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Db 66 NGG 64 Search completed: June 11, 2003, 05:00:41 Job time: 7696.77 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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2210654
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                  94.8
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2 100.0 6888 5 US-09-502-4268-1

2 100.0 6888 7 US-09-502-426A-1

4 3.5 2111522 7 US-09-947-911-63

3.1 3673778 9 US-10-312-841-1

3.1 318007 6 US-09-948-124-61

3.1 318007 6 US-09-947-911-31

3.0 245379 7 US-09-947-911-31

3.0 245379 7 US-09-947-911-31

3.0 79263 10 US-60-466-412-8416

3.0 79263 10 US-60-466-412-83408

3.0 318007 6 US-99-947-911-179

2.9 597573 7 US-09-947-911-179

2.9 4063095 7 US-09-947-911-1800

2.9 1599662 7 US-09-947-911-18

2.8 597573 7 US-09-947-911-19

2.8 7928029 7 US-09-947-911-19

2.8 7928029 7 US-09-947-911-176

2.8 31630 10 US-60-466-412-84035

2.8 31630 10 US-60-466-412-8572

2.8 4604723 7 US-09-947-916-240

2.8 656902 7 US-09-947-916-240
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

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6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*

8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*

9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*

10: /cgn2_6/ptodata/1/pna/US00_NEW_COMB.seq:*

11: /cgn2_6/ptodata/1/pna/US00_NEW_COMB.seq:*
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence 63, Appl
Sequence 63, Appli
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Sequence 61, Appli
Sequence 22, Appli
Sequence 331, App
Sequence 84116, A
Sequence 8408, A
                        Sequence 61, Appl
Sequence 17, Appli
Sequence 17, App
Sequence 51800, A
Sequence 108, App
Sequence 108, App
Sequence 17, App
Sequence 16, Appl
Sequence 84035, A
Sequence 8572, A
Sequence 240, App
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2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7
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US-09-947-911-156	US-60-466-412-86602	US-10-240-453-131	US-09-947-911-294	US-60-466-412-87958	US-60-466-412-86282	US-60-465-241-52561	US-60-466-412-86156	US-60-465-241-52473	US-09-949-016-14164	US-10-311-455-400 .	US-60-466-412-87958	US-09-947-911-254	US-60-466-412-86557	US-09-950-083B-10355	US-09-947-916-174	US-09-947-911-286	US-60-466-412-85631	US-09-947-911-231	US-60-466-412-84564	US-09-947-911-237	US-09-948-124-7	US-09-947-911-255
Sequence 156, App	Sequence 86602, A	Sequence 131, App	Sequence 294, App	Sequence 87958, A	Sequence 86282, A	Sequence 52561, A	Sequence 86156, A	Sequence 52473, A	Sequence 14164, A	Sequence 400, App	Sequence 87958, A	Sequence 254, App	Sequence 86557, A	Sequence 10355, A	Sequence 174, App	Sequence 286, App	Sequence 85631, A	Sequence 231, App	Sequence 84564, A	Sequence 237, App	Sequence 7, Appli	Sequence 255, App

ALIGNMENTS

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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
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GENERAL INFORMATION:
APPLICANT: Aspiroz, Ricardo
APPLICANT: Choe, Sunghwa
APPLICANT: Feldmann, Kenneth A.
TITLE OF INVENTION: DWF4 POLXNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: 11696-070001
CURRENT APPLICATION NUMBER: US/09/502,426B
CURRENT FILING DATE: 2000-02-11
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Best Local Similarity
Matches 3202; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 30 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/119,657 PRIOR FILING DATE: 1999-02-11 PRIOR APPLICATION NUMBER: US 60/119,658 PRIOR FILING DATE: 1999-02-11
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                241
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TAATCGATTCCATTTGGTTGGATTACACAGTTAAGTTTTTGTGTTTTCTTTTTGTTATATGT
                                                                         ATGTGGGTATTATATTGTTGGGTTCGGTTTGAGCTACAATATAAATTTCGTGTTTCTGGT
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Db 2221 CTATTTTGTTGTGGGAATGAATGATATAACATTAACAATTAATAATATAAC 2380 Qy 2281 AGCCTATACGCGCTCAAAGTATGTTATATATATAATAATAATAATAATAATAATA	Db 2041 TAAATACATTATGAACAATAATAATATGAGGAACAATAATATTTTTTTT	Qy 1921 ACATTTTAATTTAAAGACAAAATTTTTTGAAAAATGTTATAATTTCTAACAATATTAATTA		Db 1561 ATTTATTGTTAGTTGGAATTTAATAAGAGCGAACTTGTAACATTACAATATTTAG 1620 Qy 1621 ATACTAGTATGTGGAATTATTCCAAATACTTTGGAACTTTAAACTTAATCTTGTTCT 1680	Oy 1381 ATATCATTCTTGGTTGGTCAACAATAAAAACAAAAAAAAA

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APPLICANT: CHOE, Sunghwa
APPLICANT: FELDMANN, Kenneth
TITLE OF INVENTION: DWF4 POLYNUCLEOTIDES, POL
FILE REFERENCE: 2225-0001
CURRENT APPLICATION NUMBER: US/09/502,426A
CURRENT FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/119,657
PRIOR FILING DATE: 1999-02-11
PRIOR PRIOR PLICATION NUMBER: 60/119,658
PRIOR FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 25
SOPTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 6888
TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: AZPIROZ, Ricardo
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QY 3121 TCAGTAGAAGTCCGATTCCCAATCTTAAAGCCATTAGAAAGAGAAAGTGAGTG	3161 ATAACAATRATATTCTGACTTCTTTTAAACCCCCCTCTTACAAACAGAACCTCCCTTTT	3001 TGAAGCTCARTGGTTAAGTTTAATGAAGAAGATTTTATTAAATTTTAATGACGATG	2941 AAGTATTAAAAGGAGCATAACGAGGCAACAAAGTAATGAACACGGAGAAACAAAAGCCA	2881 CTATTTCAGCATCGCAGCTTTCTGCAACTTTTGTTTTTAATTTAAGAGTTTAATAAATA	2821 ACAATTGATTATAGATATATCCATTAATCCATGATATTATGATATAAATAGCTGTTAAA	761 A 761 A	2701 A 2701 A	2641 TGGGATTCTGCTGGAGCATTTATCAAAAATTATTAGCACGAATGGGTTTATTAAATTTAAA	81 1	2521 TAGGGGTCCTTCTGACATTTTCACTGTTCTACCCCTACTCGTGAGCCCACCCTTTTCCCA	61 6	2401 TTGAGTAAATGTGTTTTCTGACTATTGAGGGGCAAAAAAAA	QY 2341 TCAGAATTGGGACAACAATGAAAACGGAATTAAAATATTAACTTTAAAATAAAATAAAAAT 2400	2281 AGCCTATACGCGCTCAAAGTATGTTATCTAGTAGTCTAATTAAT	2221 CTATTTTGTTGTGGAATGGAATGTAATATACATTAAGCAAATTTTAAAAAATTATATA 	2101 IISTIANGAMAGITICAMATITITITITITITITITITITITITITITATIOGAMCANGAMATANGAMAMATANGAMAMATANGAMAMATANGAMAMATANGAMAMATANGAMAMATANGAMAMATANGAMAMATANGAMAMATANGAMAMATANGAMAMATANGAMAMATANGAMAMATANGAMAMATANGAMAMATANGAMAMATANGAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMA	2101 AAATCTACAAATTATTAATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAAA	

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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
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CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 368
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            TTATGAAAATACTGTGATTAATA 2001067
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Sequence 1, Application US/10312841
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden ger
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
LENGTH: 3673778
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 42.4%;
Matches 989; Conservative
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TGAATAATTATCAAAGAGAATA-AGAGATGACAACCAAAAGGTTGTGGAATAATGGTCCC 719
                                                    AGAGTATTGAGAAAAAACCGAAAATAAGAAAAGGGAAAGAGTAGTGACCCATGGAGTATG
                                                                                                         TAATCGATTCCATTTGGTTGGATTACACAGTTAAGTTTTTGTGTTTCTTTTTGTTATATGT 300
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Pred. No. 6.1e-07;
0; Mismatches 1320; Indels 24;
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1715022		1714963	쿵
1793		1737	Qy
1714962	TTTTATATATATTATATATATTTTGTATATATATATATA	1714903	В
1736	TAATCATCGAGGTAAAAAAAGTTTTGTCTTATTTTCGCG	1677	Qy
1714902	TATATATTTTATATGTATATATTTTATATATATATATAT	1714843	Db.
1676	TTAGATACTAGTATTGTGATTATTCCAAATACATACTTTGGATGTTTAAACTTTAATCTTGT	1617	Qy
1714842	TTATATATATTTTATATATATATATATATATATATTATT	1714783	дь
1616	ACATATTATTAGTTAGTTAGAATTTAATAAGAGCGAACTTGTAACAATATTTATA	1557	όy
1714782	TGTATATTTTATATGTATATTTTATATATATTTTATATGTATATTTTATATATATATATATATAT	1714723	DЬ
1556		1497	Qy
1714722	ATATTTTATATATATTTTATATGTATATTTTATATGTATATTTTATATGTATATTTTATA	1714663	рь
1496	CTTTTGGGTTACAGTTTCGAA	1437	Qy
1714662	ATATATATATATATATATATATATATATATATATATAT	1714603	Дb
1436	GCAAATATCATTCTTGGTTGGTCAACAATAAAAAACAAAAAACAAGAAAAAAAA	1377	Qy
1714602	TATATATTTTATGTATATATTATATATATATATTTTATGTATATTTTAT	1714550	Дb
1376	TGTCGATAAATGAAATTCACACGCGTGGTAATAATTATGGGACCGTATGTTACGATCACT	1317	Qy
1714549	ATATATTTTATATATATTTTTTATATATATTTTTATATAT	1714490	Db
1316	CACGTATGCTATACTAGAGACTAAAGAATAGTTATGTGA	1257	Qy
1714489	TATATATTTTATATATATTTTATATATATTTTATATATAT	1714430	Db
1256	GTCAACATATACATAATTCCTTACAGAAAAAACAAACTTAAGAGAAGTTAACATATCCAT	1197	Qy
1714429	ATATATATTTTATATATATATTTTATATATATATATAT	1714370	Db
1196		1137	Qy
1714369	TATATATTTTATATATATTTATATATTTTATATATATA	1714310	Db
1136	AAGCTATTTATACAAAGTTACAAACTGAATATAGCTTGAAATCCTTTAGAAAATTTTGGA	1077	Qy
1714309	TTTTATATATATTTTATATATATATATATTTTATATATAT	1714250	Db
1076	ACGATTTTACAGCGTCACTAGTTGAGATTACTAGCATAAAGCATAAAGGACCCGTTC	1020	Qy
1714249	ATATATATTTTATATATATATATATATTTTATATATTTTATA	1714190	Db
1019	GACCATTTTGAATAAACTTTTTCTCAAACATTACGGGACACTGGACTCGACCCTTAAAAT	960	Qy
1714189	TATATTTTATATATATATTTTATATATATATTTTATATATA	1714136	Db
959	GATAACAATGATATATCACAAAACAATTGTCTGG	900	Qy
1714135	ATATATTTATATATATATTTTATATATATTTTATATATAT	1714076	Db
899	AGGTATTTGCATAATCTTCTGTTTAAAGCATATTTTGTCTTTTTTTT	840	Qy
1714075	TATATATTTTATATATATTTTATATATATTTTTATATATA	1714016	Db
839	ATTTGCGATAACGATTGTGAAAAATATTTTATTTGTTAGCTGATCTCAATATTATGTTCC	780	Оу
1714015	ATATATATTTATATATATATATATATATATATATATAT	1713956	DЬ
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GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden
FILE REFERENCE: E01/1208/WO
                                                                                                                                                                 Matches
                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: unsure
LOCATION: (3294164)
                                                                                                                                                                                                                                                                                                                LENGTH: 3673778
TYPE: DNA
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OTHER INFORMATION:
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Pred. No. 1.6e-06;
0; Mismatches 1218;
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RESULT 6
US-09-948-124-61/c
; Sequence 61, Application US/09948124
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
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TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED TITLE OF INVENTION: Y, METHODS OF DETECTION, AND USES THEREOF FILE REFERENCE: CL001301
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CURRENT FILING DATE: 2002-12-23
NUMBER OF SEQ ID NOS: 183
SEQ ID NO 61
LENGTH: 318007
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
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Best Local Similarity
Matches 735; Conservat
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                                        CAATGATCTAAAATGCATAGATCTTTTGGGTTACAGTTTCGAAGTCCTCTACAAGCGTGT 1513
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                                                                                        TTGGTCAACAATAAAAACAAAAACAAGAAAAAAAAAGAAAACGATTTTTCTTGGATTCCATT 1453
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Pred. No. 3.1e-06;
0; Mismatches 891;
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RESULT 7
US-09-947-911-2/c
; Sequence 2, Application US/09947911
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                                                              GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM
TITLE OF INVENTION: X, METHODS OF DETECTION, AND USES THEREOF
FILE REFERENCE: CL001300
CURRENT APPLICATION NUMBER: US/09/947,911
CURRENT FILING DATE: 2001-09-07
                                         NUMBER OF SEQ ID SEQ ID NO 2
                 LENGTH: 60
   ORGANISM: HUMAN
                              600322
                                                                                                                                                                                                                     TATATATAAATATTAAATATAATA 133367
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; LOCATION: (1)...(600322)
; OTHER INFORMATION: n = A
US-09-947-911-2
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                       TGGAATTTAATAAGAGCGAACTTGTAACATTACAATATTTATATTAGATACTAGTATGTG 1633
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ACATGATATATTATTATACCATATTATATTATATGTAATAATATATTGATTATTATAT
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Pred. No. 2.8e-06;
0; Mismatches 891;
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; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2453797)
; OTHER INFORMATION: n = A,T, US-09-947-911-331
                                                                                                                                                                                       US-09-947-911-331

Sequence 331, Application US/09947911

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED
TITLE OF INVENTION: X, METHODS OF DETECTION, AND USES THEREOF
FILE REFERENCE: CL001300
CURRENT APPLICATION NUMBER: US/09/947,911
CURRENT FILING DATE: 2001-09-07
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    Matches 469; Conserv
               Query Match
Best Local :
                                                                                                                                    NUMBER OF SEQ ID NOS: 368
SEQ ID NO 331
LENGTH: 2453797
TYPE: DNA
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Score 97.4; DB 7;
Pred. No. 4.3e-06;
0; Mismatches 561;
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                         Length 2453797;
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                                       TATTGAGGGGCAAAAAAAAGACAAT 2447
                                                                  AACGGAATTAAAATATTAACTTTAAAATAAATAAAATTTGAGTAAATGTGTTTTCTGAC 2422
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; Sequence 84116, Application US/60466412;
; GENERAL INFORMATION:
; APPLICANT: CARCILL, Michele
; APPLICANT: IAKOUBOVA, Olga
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CURRENT FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 429241
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 84116
LENGTH: 23939
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 363; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION FILE REFERENCE: CL001466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                                   CCAATAATAGTTGGTGAATTCAAATATCTCCATTAATATTTTTTTGA---AATCTACAAAT 2112
                                                                                                                                                                                                                                             CTCAAAGTATGTTATCTAGTAGGTGTAAT--TAATAATGCATGGTGCGATTCAGAATTGG
                                                                                  GGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCG
                                                                                                                     GACAAAATTTTTGAAAAATGTTATAATTTCTAACAATATTATTAAAATATGATGCCTATA 1995
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ilarity 49.4%;
Conservative
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Pred. No. 1.1e-05;
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Best Local
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; ORGANISM: Homo sapiens US-60-466-412-83408
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CURRENT FILING DATE: 2003-04-30
NUMBER OF SEO ID NOS: 429241
SOFTWARE: FAStSEQ for Windows Version 4.0
SEQ ID NO 83408
LENGTH: 79263
TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olya
TITLE OF INVENTION: MUCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001466
                                                          40522 AATTATTATAATATAAATATGCATATACTATAATAATATCTATACTATAAAATATATTT 4058:
                                                                                                                                                                                                                                                                                                                                                                                              1645 TACATACTTTGGATGTTTAAACTTAATCTTGTTTCTTCCTACGGTATAAATATTAATCAT 1704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1405 TAAAAACAAAAACAAGAAAAAAAGAAAACGATTTTTCTTGGATTCCATTCAATGATCTAA 1464
GTTGGTGAATTCAAATATCTCCATTAATATTTTTTGAAATCTACAAATTATTAATATTTA
                                                                                                    CTATGTTCTTAAAATATTTTTTTTTTATATTTAGTTATAAATACATTATGAACCAATAATA
                                                                                                                                                                                                                            CAATGCTACTATCAATAGAAGAAACAGCTGAGTATTACATTTTAATTTAAAGACAAAATT 1944
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Similarity 46.2%;
                                                                                                                                              TATAAATATACATGTAATATGTAAATATA-TATAATTTATAAATATACATATACTATGTA
                                                                                                                                                                                     TTTGAAAAATGTTATAATTTCTAACAATATTATTAAAAATATGATGCCTATAATGTATTTC 2004
                                                                                                                                                                                                                                                                                                             TAA-----ATGCATATTTATAATATATATAACTATGCATATATGTAAATATGTAATAATA 40400
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGAGCGAACTTGTAACATTACAATATTTATATTAGATACTAGTATGTGATTATTCCAAA 1644
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Pred. No. 1.2e-05;
0; Mismatches 530;
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US-09-948-124-61
; Sequence 61, Application US/09948124
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
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NAME/KEY: misc_feature
LOCATION: (1)...(318007)
OTHER INFORMATION: n = A,'
IS-09-948-124-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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SEQ ID NO 61
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CURRENT FILING DATE: 2002-12-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity 46.5%;
 CTACTATCAATAGAAGAAACAGCTGAGTATTACATTTTAATTTAAAGACAAAATTTTTGA 1949
                             АТАЛАПАЛАПАТАПАТАСТТАПАЛАПАЛАПАТАТАЛАПАЛАПАТАЛАЛАТАТАЛАТАТАЛАЛАЛА 133719
                                                           ACAGCCTCTACAACTGTGATAGTCAATTTTTTCTGCAAATATTAAATTAGGAATTCAATG 1889
                                                                                            TAAAAAAAGTTTTGTCTTATTTTCGCGATGCATGAAGGATAAACCTAATGACTTTAATTT 1769
                                                                                                                                                                                                                        CGAACTTGTAACATTACAATATTTATATTAGATACTAGTATGTGATTATTCCAAATACAT 1649
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                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 318007;
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; LOCATION: (1)...(600322)
; OTHER INFORMATION: n = A
US-09-947-911-2
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SEQ ID NO 2
LENGTH: 600322
TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED
TITLE OF INVENTION: X, METHODS OF DETECTION, AND USES THEREOF
                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 411; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: CL001300
CURRENT APPLICATION NUMBER: US/09/947,911
CURRENT FILING DATE: 2001-09-07
                                                                                                                                                                                                                                                                                                                                  ORGANISM: HUMAN FEATURE:
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                                                                                                                                                           1530 TAAATTGCTTTTAATGCATCTTTAACATATTTATTGTTAGTTGGAATTTAATAAGAG 1589
                                                                            ACTITGGATGTTTAAACTTAATCTTGTTTCTTCCTACGGTATAAATATTAATCATCGAGG 1709
                                                                                                         CGAACTTGTAACATTACAATATTTATATTAGATACTAGTATGTGATTATTCCAAATACAT 1649
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Pred. No. 1.3e-05;
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                                                                                                                CURRENT APPLICATION NUMBER: US/09/947,911
CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 368
SEQ ID NO 179
LENCTH: 597573
TYPE: DNA
ORGANISM: HUMAN
                                                                                                                                                                                                       Sequence 179, Application US/09947911
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: COLLECTION OF SINGLE NUCLECTIDE POLYMORPHISM (SNPs) LOCATED ON
TITLE OF INVENTION: X, METHODS OF DETECTION, AND USES THEREOF
FILE REFERENCE: CL001300
                              Query Match
                                                   NAME/KEY: misc_feature
LOCATION: (1)...(597573)
OTHER INFORMATION: n = A
-09-947-911-179
                                                                                                      FEATURE:
     Local Similarity
nes 519; Conserv
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              Score 94.2; DB 7; Pred. No. 1.6e-05;
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                                                          AGTCAATAACAATGCATAGAAAAGTTCCAAAATTTTGTTAACAGAAACTTCCAAATT
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NAME/KEY: misc_feature

: LOCATION: (1)...(4063095)

: OTHER INFORMATION: n = A,T,C

US-09-947-911-323
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SEQ ID NO 323
LENGTH: 4063095
TYPE: DNA
ORGANIAM: HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED TITLE OF INVENTION: X, METHODS OF DETECTION, AND USES THEREOF FILE REFERENCE: CL001300
CURRENT APPLICATION NUMBER: US/09/947,911
CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 368
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1414885
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Pred. No. 2.1e-05;
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            TCTTATTTTCGCGATGCATGAAGGATAAACCTAATGACTTTAATTTTTTGAAAATGTAAC
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APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASS
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, MI
FILE REFERENCE: CL001468
CURRENT APPLICATION NUMBER: US/60/465,241
CURRENT FILING DAYE: 2003-04-23
NUMBER OF SEQ ID NOS: 258418
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 51800
LENGTH: 1202549
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                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(1205549)
OTHER INFORMATION: n = A,T,C
-60-465-241-51800
                                                                                                                                                                                                   ORGANISM: Homo sapiens
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ALIGNMENTS

JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE RESULT 1 AL768954 LOCUS REFERENCE AUTHORS VERSION KEYWORDS SOURCE ORGANISM ACCESSION DEFINITION TITLE JOURNAL Arabidopsis thaliana T-DNA flanking genomic survey sequence.
AL768954 Unpublished
3 (bases 1 to 473)
1 (bases 1 to 473)
Li, Y. Rosso, M., Strizhov, N. and Weisshaar, B. Direct Submission and Weisshaar,B.
A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA thale cress.
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; Brassicaceae; Arabidopsis. Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics Unpublished Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H. GSS AL768954.1 transformed lines AL768954 GI:21522073 DNA linear GSS 18-JUN-2002 sequence GK-082A08-011867,

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                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Brassicaceae; Arabidopsis.
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                                                           1 to 148)
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and Ecker,J.R.
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Parker, H., Prednis, L., Shinn, F
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               (bases 1 to 473)
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   Strizhov, N.
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TITLE
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The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
                                                                                                                                                                                                A pipeline for automated
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Arabidopsis thaliana T-DNA flanking
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Unpublished (2001)
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/db_xref="taxon:3702"
/clone="sALK_057128"
/clone_lib="Arabidopsis thaliana_TDNA_insertion_
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Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion within the locus defined by clone T3A5. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.

    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was
collaboration with the Berkeley Drosophila
The BDGP is constructing a physical map of

                                                                                                                                                                    Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster genome survey sequence T7 end of BAC: BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 TTAC 3
                                                                          Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                    Genoscope.
                                                                                                                                                                                                                                                                            GSS
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BDGP is constructing a physical map of
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                                                                                                                                                                                                                                                                                                                                genomic survey sequence.
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/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thalaina nuclear genome sequence were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             processed for submission. T-DNA derived sequences were
removed"
1 58 c 70 g 146 t 31 others
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/clone="GK-082A08-011867"
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survey sequence T7 end of BAC
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    the Drosophila
                                        carried out as
                                                                              segref@genoscope.cns.fr
                                                                                              National de Sequencage
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                      Genome Project
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1925 TTTAATTTAAAGACAAAATTTTTGAAAAATGTTATAATTTCTAACAATATTATTAAAAATA 1984
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500 TTTTTWATTWATAAWITTWTTTWWAWATTWWKKKKKKAWADTGAGARA 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               800 WITWIATTWIATAWWWIWWAIWWWIAWAAWTAIATAIWWATATIAIWWIWAITWII 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Nr. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 180genic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/note="end: T7"
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/db_xref="taxon:7227"
/clone="BACR29B23"
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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AL069706.1 GI:4949849
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                                                                                    AATATTAATCATCGAGGTAAAAAAAGTTTTGTCTTATTTTCGCGATGCATGAAGGATAAA 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                         GATTATTCCAAATACATACTTTGGATGTTTAAACTTAATCTTGTTTCTTCCTACGGTATA 1692
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/note="end : T7"
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila NAM provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers
1808
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fly), genomic survey sequence. AL061936
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GTATGTTTTTGTTGCCATAATGACAGCCTCTACAAC ---TGTGATAGTCAATTTTTTCTG 1864
                                                         AMAMAMCMAWTATHTTHAAACTCTMTTHTTTTMTTYTMTMTTCTCTTTTTTTTTTTTTT 1038
                                                                                                               SERVICE SERVIC
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/db_xref="taxon:7227"
/clone="BACR05N11"
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/note="end : TET3"
7 c 28 g
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43.98;
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                                                                                                                                                                                                               Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) ttp://www.edgp.ebi.ac.uk This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fly), genomic survey so
AL099642
AL099642.1 GI:5611253
GSS.
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN05N18 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                       Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
                                                                                                                                                                                                                                                                                                                                                                          Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
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                                                           /clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : T7"
a 58 c 42 g ;
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                                                                                                                    /organism="Drosophila
/db_xref="taxon:7227"
/clone="BACN05N18"
                                                                                                                                                                                  ocation/Qualifiers
3.1%;
Score 98.4; DB 17
Pred. No. 5.8e-05;
                                                                                                                                                    melanogaster
                                                            269
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              DB 17;
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            Length 836;
                                                            others
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collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the
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Determination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of Determination of Determ
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   Gu, J.,
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/ob_xref="taxon:7227"
/clone="BACR29p01"
/clone_lib="RPC1-98"
/note="end : TET3"
a 66 c 104 g :
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               Eutheria;
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   Liu, F., Qu, J.,
                               Chordata;
Primates;
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Pred. No. 5.
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 Zhao, M.,
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                               Vertebrata; Euteleostomi;
i; Hominidae; Homo.
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Chinese National Human Genome Cent
351 Guo Shoujing Road, Zhangjiang
201203, P. R. China
Tel: 86-21-50801919(ex.45)
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Homo sapiens CDNA DCB clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 86-21-50801922
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   CCAAATTTTTTTTTTTTTTGGAACAAGAAATAACAGATAGAAAACTATTTTGTTGTGGAA
                                                                                                                                      CAATAATAGTTGGTGAATTCAAATATCTCCCATTAATATTTTTTTGAAATCTACAAATTATT
                                                                                                                       ATTAAGTCAAATTTTATTTTTTATGTTTATTACTTATTGGATAATATAAGGTC
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                                                             AATAGAAACTCCTATAGAAAAAGATAAATGAATATATAAATTAAATTATACGTATTTG
                                                                                         TGTATTTCCTATGTTCTTAAAATATTTTTTTTTTATATTTAGTTATAAATACATTATGAAC
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clone is available
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/lab_host="BM25.8"
/lab_host="BM25.8"
/note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB"
/note="Vector: 20 g 345 t 4 others
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/db_xref="taxon:9606"
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46.28;
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Best Local Similarity
Matches 176; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-APR-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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Tetraodon nigroviridis genome surve
222L11 of library G from Tetraodon
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                                                                                                                                                                                    CCATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTTCTGCAAATATTAAATTAGGA 1881
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                                                                  ATTTTTGAAAAATGTT--ATAATTTCTAACAATATTATTAAAATATGATGCCTATAATGT
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/note="Genoscope sequence ID : C0AG222CF06LP1-end :
/note="Genoscope sequence ID : C0AG222CF06LP1-end :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:99883"
/clone="222L11"
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Pred. No. 5.7e-05;
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                                                                                                                                                                                        1640 CCAAATACATACTTTGGATGTTTAAACTTAATCTTGTTTCTTCCTACGGTATAAATATTA
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 1101)
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BACROBKOB of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                               ATCATCGAGGTAAAAAAGTTTTGTCTTATTTTCGCGATGCATGAAGGATAAACCTAATG
                                                                                                                                                   CCGATTCTTTAATHAACAACTHCCAAACCCCTTYTCYCMCCMCMMMMMMAAAAAAAAA
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/note="end : TET3"
/note="end : TET3"
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/db_xref="taxon:7227"
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                                                                                                                                              - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster genome survey sequence T7 end of BAC BACN15M24 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                      Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.f.
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/clone_lib="DrosBAC"
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygóta; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
   Genoscope.

Direct Submission

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)
                                                                                                                                                          Drosophila melanogaster.
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1 87 c 79
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Pred. No. 0.0002;
                                                                                                                                                                                                                                                                                     1101 bp
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Insecta; Pterygota;

Muscomorpha;

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GTATGTTTTTGTTGCCATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTCTGCAA 1867
                                         AGAATTGGGACAACAATGAAAACGGAATTAAAATATTAACTTT 2385
                                                                                     CAAAMAAAAMAMAAATAAAMAAAATCTAKKNDKKKWAADAKDDNAKASAWGBKKMMAATW
                                                                                                                               GTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAA.----TTATATAAG
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                                                                                                                                                                             TTTHACAAMMAMMAMMYMMMCAAAAMAMMAAVMAAAMACMAMMMTAAAGCNTAAAAAAA
                                                                                                                                                                                                                                                                                                            CAGAAACTTCCAAATTTTTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAACTATTTT
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RESULT 14
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             Drosophila melanogaster Drosophila melanogaster
                                                           fly), genomic survey sequence.
AL069440
AL069440.1 GI:4949583
GSS.
                                                                                                                                      Drosophila melanogaster genome sur
BACR29P01 of RPCI-98 library from
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/note="end : TET3"
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/db_xref="taxon:7227"
/clone="BACR08K08"
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42.8%;
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Pred. No. 0.00024;
il; Mismatches 218;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2045 TACATTATGAACCAATAATAGTTGGTGAATTCAAATATCTCCCATTAATATTTTTTTGAAAT 210
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900 AATGWTTTWTAAATTWWGTTAWTTTTTATTTTWAAATTGTATATAAAAAWWATTATGTA 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425 ACATKAAWAAARRGGGGAKAAATAWTTKGAAAGATATAAAAAAAAAAAAATAWTAA
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                              TAACAGAAACTTCCAAATTTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAA-----A
                                                                                                                                                                                                                                                                                                                                                                                  CTACAAATTATTAATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTTTTGT 2164
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                                                                                                                                                                                                                                                       TATAAATAAWWWATKTTTTTATWWWATATAAAAWAATTTAATTTTTWATTTTATATATT
                                        WAAAAAAATNWTATAAWATTWWKAATAATWTATAWWTTTAWATATWATRTAAATTWTAA
                                                                                    TWYTTTTTWTTTAWTTTAAWATTTTTTTAWWTAAWAWTGTAATWAAATTAWWTTAAAAAW
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/db_xref="taxon:7227"
/clone="BARR299D1"
/clone_lib="RPCI-98"
/note="end : TET3"
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Pred. No. 0.00024;
3; Mismatches 269
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	929 ATTTAAAGACAAAATTTTTGAAAAATGTTATAATTCTAACAATATTATTAAAATATGAT 198 :	ов 29
	1869 TATTAAATTAGGAATTCAATGCTACTATCAATAGAAGAACAGCTGAGTATTACATTTTA 1928	Db Dy
	1809 TATGTTTTTGTTGCCATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTCTGCAAA 1868 	Db Dy
	Match 2.9%; Score 93; DB 17; Length 1101; Local Similarity 39.2%; Pred. No. 0.00029; Les 235; Conservative 78; Mismatches 278; Indels 8; Gaps 1;	Query Ma Best Low Matches
	/organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone="BACR24D09" /clone_lib="RPCI-98" /note="end: T7" 420 a 56 c 48 g 261 t 316 others	BASE COUNT
	EcoRI digestion of Drosophila DNA provided by the BDGP flaggenic strain y2; on bw sp, the same strain used for tpl and EST libraries. A more detailed description of the and how to order individual BAC clones, the entire libra filters for hybridization from the BACPAC Resource Center found at http://bacpac.med.buffalo.edu/drosophila_bac.ht location/Qualifiers	FEATURES SOUTCE
	sophila information phila osoegawa and Osoegawa and the Department ite in Buffalo	
	carried out	COMMENT
		AUTHORS TITLE JOURNAL
	Drosophila Eukaryota; Neoptera; E Ephydroidea 1 (bases 1	ORGANISM REFERENCE
•	fly), genomic survey sequence. AL057419 AL057419.1 GI:4937885 GSS. Drosophila melanogaster	ACCESSION VERSION KEYWORDS
	C (NS00BO1 1101 bp DNA linear GSS 04-JUN-1999 NN Drosophila melanogaster genome survey sequence T7 end of BAC # BACR24D09 of RPCI-98 library from Drosophila melanogaster (fruit	RESULT 15 CNS00BO1/c LOCUS DEFINITION
	2460 CGGGTTTGA 2468 : : : 1020 GTRTWIKWA 1028	ъ <i>у</i>
	2400 TTTGAGTAAATGTGTTTTCTGACTATTGAGGGGCAAAAAAAA	ОУ

			<u> </u>
96	4 ATTAAAARSATAARAAATTAKTRAAAAAAATATTTGTKGTKGTTTTTADTTWDWTTA 506	b 564	dα
407	9 GGGACAACAATGAAAACGGAATTAAAATATTAAACTTTAAAAATAAAAATATTTGAGTA 2407	у 2349	Qy
565	624 TTTASTSSATAATTATTSVTRATTGVTTDAWTTTAAARSAAAAAAKTTTRBAAAAAAAA 565		םם
2348	9 CGCGCTCAAAGTATGTTATCTAGTAGGTGGTAATTAATAATGCATGGTGCGATTCAGAATT 2348	N)	γo
625	4 WISTAMAATSVCASBSSVWTTATATTTTTTASAAAWAWAKAWAATTTTSTGSTRTTTATT 625	b 684	αd
2288	9 TTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAAATTATATATA	y 2229	Qy
685	4 AAAWATAAAAAMAAATTTTTTTTTTTTTATAAASVMTWKVMASSSCAATVTWAWAAATAA 685	b 744	ф
2228		у 2169	у
745	WAATWATTTTTTTTTTTTTWAWTTAATTTATATAAATTAATAWAWWAW	b 804	Db
2168	9 AAATTATTAATATTTAGTCAATAACAATGCATAGAAAGGTTCCAAAAAAAA	у 2109	Qy
805	6 TTAAATTTATAWAWTWATTATWTTTTATTTTTTTT	b 856	Db
2108	TTATGAACCAATAATAGTTGGTGAATTCAAATATTCTCCATTAATATTTTTTTGAAATCTAC	у 2049	Оу
857	916 ATAAWAATTATTTTAATATTWTTTAAATAAATTTTWTTTTATTTWTWTTTATTA		dg b

Search completed: June 11, 2003, 06:58:37 Job time: 4856.18 secs

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GenCore version.5.1.6
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OM nucleic - nuc	nucleic search, using sw model
Run on:	June 10, 2003, 22:00:04; Search time 2933.8 Seconds (without alignments) 10921.753 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-502-426B-1_COPY_2102_3202 1101 1 aatctacaaattattaatatgagagagagagaaactaqctcc 1101
Scoring table:	
Searched:	2054640 segs, 14551402878 residues
Total number of }	hits satisfying chosen parameters: 4109280
Minimum DB seq le Maximum DB seq le	seq length: 0 seq length: 200000000
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	GenEmbl:* 11 9b_ba:* 21 9b_ba:* 22 9b_ba:* 31 9b_ba:* 32 9b_ba:* 33 9b_in:* 4 9b_om:* 5 9b_ba:* 5 9b_ba:* 6 9b_pat:* 10 9b_pat:* 11 9b_sat:* 11 9b_say:* 12 0b_vi:* 13 9b_un:* 14 9b_vi:* 15 0m_ba:* 16 0m_on:* 17 0m_sa:* 18 0m_ni:* 18 0m_ni:* 19 0m_ni:* 10 0m_ni:* 11 0m

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AF044216 Arabidops	AF273674 Plasmodiu	AE001372 Plasmodiu AC117079 Dictyoste	Tome	ACUZU341 HOMO SAD1 AC094291 Rattus no	Homo sa	AL034559 Plasmodiu AC114238 Rattus no		AC11/0/Z Dictyoste AC115575 Dictyoste	AC004157 Plasmodiu	ALUZI483 Caenorhab AC009224 Homo sapi	AC109656 Rattus no	AL109954 Human DNA	AL032644 Caenorhab	AC004153 Plasmodiu	AC116550 Dictyoste	AX252043 Sequence	AX344427 Sequence	AC115598 Dictyoste	ALO31746 Plasmodiu	AC016220 Homo sapi	AC023122 Homo sapi	AL390756 Homo sapi	Continuation (3 of	ALLZIBUB Human chr AC087071 Homo sapi		Dicty	ACO04709 Plasmodiu	<u></u>	Arzunszi Plasmodiu AE001398 Plasmodiu		DNA. linear PLN 25-JUN-2001	-alpha-hydroxylase (DWF4) gene,			diplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; dis II; Brassicales; Brassicacee: Arwhidons;	Takatsuto, S., Sakurai, A. and
SUMMARIES	AF044216 ATT3A5	AF273674	AC117079	TSP418778	AC094291	AL732314 DEWAL3D7	AC114238	AC007182	AC115575	AC004157	AC009224	AC109656 AC116985	HSJ333B15	CEY51H1A AC005504	AC004153	AC117082	AX252043	AX344427 AX348822	AC115598	PFMAL1P3 AC127730	AC016220	AC023122 PFMAL3P1	AL390756	PEMAL13P2_2	AC087071	AC073320	AC115613 AC006280	AC004709	AP000807	AE001398	ALIGNMENTS	4818 bp Dr	steroid 22	- +		tae; Streptophyt iophyta; eudicot Brassicales; Br	Fujioka, S., Tak
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ATT3A5 84196 bp DNA linear PLN 26-JAN-2000
Arabidopsis thallana DNA chromosome 3, BAC clone T3A5.
AL132979
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 84196)
Bloecker,H., Mewes,H.W., Lemcke,K., Mayer,K.F.X., Quetier,F. and
 GGTTTGACTGTCCAGTTCGGTAATAATCTAATAACTCTGTCTTTGACCGCACGCTCGTGT
                                                                                                                                                                  AGGGGTCCTTCTGACATTTTCACTGTTCTACCCCTACTTGTGAGCCCCACCCTTTTCCCAT
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WORPFIGGETICYLKPYTATIOPWQDYBKYGKY KTRNLEGEPTIVSADAGLNRFTLQ
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TLFVLDSWQONSIFSAQDEAKKFTFNLMAKHTNSMDPGEEETEQLKKEFYJFFNKGVYS
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      The DWF4 gene of Arabidopsis encodes a cytochrome P450 that mediates multiple 22alpha-hydroxylation steps in brassinosteroid biosynthesis
Plant Cell 10 (2), 231-243 (1998)
98158690
2 (bases 1 to 4818)
2 (bases 1 to 4818)
Choe, S., Dilkes, B.P., Azpiroz, R. and Feldmann, K.A.
Direct Submission
Submitted (22-JAN-1998) Plant Sciences, University of Arizona, tucson, Az 85721, USA
                                                                                                                                                                                                                                                                                                                                                                                           join(<1133. 1353,1434. 1758,1844. 1996,2095. .2409,
2562. .2654,2746. .2824,2931. .3040,3795. .4398)
/gene="DWR4"
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2562. .2654,2746. .2824,2931. .3040,3795. .404
/gene="DWF4"
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990. .4398
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/gene="DWF4"
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Feldmann, K.A.
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MPSADFAFSVTDYSMIPADEIFLKGKILPFKETSHVHRTLGEELLTEEEGSMVDGNTF
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/note="Contains Cytochrome P450 cysteine heme-iron ligand signature AA455-464;Prokaryotic membrane lipoprotein lipid attachment site AA320-330"
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/gene="T3A5.40"
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                                                                               Direct Submission

We submitted (25-JAN-2000) MIPS, at the Max-Planck-Institut fuer
Blochemie, Am Klopferspitz 18a, D-83152 Martinsried, FRG, E-mail:
Blochemie, Am Klopferspitz 18a, D-83152 Martinsried, FRG, E-mail:
lemckedmips.blochem.mpg.de,mayer@mlps.blochem.mpg.de Project
Coordinator: Marcel Salanoubat and Francis Quetier, Groupement
d'Interet Publish, Centre National de Sequencage - GENOSCOPE; 2 rue
http://www.genoscope.cns.fr
On Jan 27, 2000 this sequence version replaced gi:6434247.
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/.
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KEAELEDFFQVAEKDLRNKILDECSMKYNFDFEKDEPLGGGRYEWVKLNP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"similarity to cyclin-dependent kinase inhibitor
(ICKI), Arabidopsis thaliana, EMBL:ATU94772_1"
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//note="similarity to predicted proteins, Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                      1. .84196
/organism="Arabidopsis thaliana"
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/db_xref="GI:6561967"
                                                                        sequencing, project.
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7565. .7922
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/db_xref="taxon:3702"
/chromosome="3"
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12339. .13197
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/gene="T3A5.10"
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Salanoubat, M.
Unpublished
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29741 GGTTTGACTGTCCAGTTCGGTAATAATCTAATAACTCTGTCTTTGACCGCACGCTCGTGT 29682
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                                                                                                                                                                                                                                                                                             29681 AGGGGTCCTTCTGACATTTTCACTGTTCTACCCCTACTCGTGAGCCCACCCTTTTCCCAT
                                                                                                        ACTCACAACTTGATCAGATAAAATTTCATAAACACTTTTTACGATGGATTCGTACGATCTA
                                                                                                                                                                                                                                 TCTAATGACTTTTTTTTTTTTCTACCACGGTGGATGAAAGTTATAGTACTATTAGCCAGAGA
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Li.J., A., Maga,J.A., Cermakian,N., Cedergren,R. and Feagin,J.E.
Direct Submission
Submitted (31-MAY-2000) Seattle Biomedical Research Institute,
                              AGGGTCCTTCTGACATTTCACTGTTCTACCCCTACTCGTGAGCCCACCCTTTCCCAT
                                                                                                                                                    GGGATTCTGCTGGAGCATTTATCAAAATTATTAGCACGAATGGGTTTATTAATTTAAAA
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                                                                                         ATCCTAAGGGTAATTTTGGAAATCCCAATTTAAACCGATTGAGACCGTACCGGACTTCCT
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VPNWRPRRLGGGLGTSRVGGEEIVGEQQPQGRTSQSEEPSRPREERKSKRERE
RSRELSHEQPRERSKRENDRFRENKHRRDNGGRDRDRDRTSRDRFRERKGKRERE
GRORTSRDHDRDRSRKKENDYFEGGEYEHGGGGRSRENDAEYRGEPEETRGYYEDDGGD
TDRYSHRYDKWEEDDFRYEREYKRSKRSESREYVR"
// OMPLEMENT (38307) 38796)
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                                                                                                   38307. .41323

4040ce—7335.50"

complement(join(38307. .38796,38877. .39090,39189. .39270,

40180. .40242,40337. .40401,40489. .40564,40655. .40734,

40805. .40919,41225. .41323))

/note—"Contains Eukaryotic putative RNA-binding region

RNP-1 signature AA179-186"
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Pred. No. 1.9e-178;
O: Mismatches 0;
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           complement(28374. .28698)
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complement(40243. .40336)
/number-4
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complement(38877.
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                                                                                                                                                                                                                 /codon_start=1
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                                                                                        'number=8
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Best Local Similarity 99.9
Matches 1101; Conservative
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IFESISEIFKRAMIIKKWFNNLSKVTNELNIPITWISPIGLPCEQPYRLGNRILVNTP
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WAHACNVDIMNQFIRESFITLYNEPILENIYNNFRIRLGKFAFKIPSSPEQGELDISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 IGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGC
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5.7%; Score 62.6; DB 3; Length 4629;
Best Local Similarity 48.2%; Pred. No. 0.16;
Matches 176; Conservative 0; Mismatches 189; Indels 0
                                                                                                                                                                                                                                                                                                                                               /product="DNA-dependent RNA polymerase"
70. .4581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="DNA-dependent RNA polymerase"
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                                                                                                                                                                                                         /note="west African origin"
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/gene="TRNAP"
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/gene="TRNAP"
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AE001372 12029 bp DNA linear INV 16-APR-2002 Plasmodium falciparum chromosome 2, section 9 of 73 of the complete
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Plasmodium falciparum 3D7.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
Gardner,M.J., Tettelin,H., Carucci,D.J., Cummings,L.M., Aravind,L., Koonin,E.V., Shallom,S., Mason,T., Yu,K., Fujii,C., Pederson,J., Shen,K., Jing,J., Aston,C., Lai,Z., Schwartz,D.C., Pertea,M., Salzberg,S., Zhou,L., Sutton,G.G., Clayton,R., White,O., Smith,H.O., Fraser,C.M., Adams,M.D., Venter,J.C. and Hoffman,S.L.
311 IGTITICTGACTATTGAGGGGCAAAAAAAAGACAATGCCAAAAGTCTACGGGTTTGACTG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (02-NOV-1998) The Institute for Genomic Research, 9712
Medical Center Drive, Rockville, MD 20814, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="knob-associated His-rich protein"
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gene="Prepolition"

complement(join(1505. 3358,3806. 3916))

/gene="Prepolition"
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    12029
    organism="Plasmodium falciparum 3D7"

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complement(7684. .8322)
/gene="PFB0105c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="predicted by GlimmerM"
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99021743
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AE001372.1 GI:3845094
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Gardner, M.J.
                                                                                                             2483 GTCAG 2487
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DEFINITION
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KEYWORDS
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/product-"hypothetical protein"
/product-"hypothetical protein"
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/product-"hypothetical protein"
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QRRGNNYINGCANUMNLKTRELAQKAMLFERTLHQRQII"
complement(join(2740 .3021,3124 .3357,3454 .3626,
7,001="0FF-ID:dd_02312"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"MYTDVSDSLSKFIIVRTILSGSFRCARVRRMALCEIESNAFSKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIFLEKSKGDRRTISKLENYEINKEDFKMLDLIKQSIRANNFTAVKFFSGGDNEENDG
YQLQIYPSTLKCALLSKDLEIIKYIFNNLILYNIENNFKGIGLNGLLKIITTTTTTT
TTTTTTTTTTTTTKQNKDNEIIEFLIEKFQSIDSDQLKETIDLNYLIMETKNYELIDKI
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RIETVNYLLSNYLQELTNOGPLKTYYTIPOFNNLSILNIFLSNEIYKSLLALYEINSE
IQYSDSESFKFINGTYEKDFYNKSFKYGYLSICKLLEEHYGSNNNNNQDNNSENSSSN
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EKLNRNSNGGYVELTPISQSKRQRKNIGNRLVRPCDCKGTQRHVHVKCLCEWIGKCNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mannnnnnnnnenkneylfwkyfknkyliknifyQmtiennefn
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ELEKRIFERIYSSLILDSTILNNLDSLKSTYRFILKGFERQFELLLQLFKRFGNNEHYO
DELIFKRYDENNHQDDFKIIKDIFNFNNWYISKHFFNNIIKCLTSSKEFSLKEKEK
LIKRINFTRYPKSSLKIVFLNLQKNFNISKLILSRIIDNNNNNGDDGDDGVVDIFN
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LYEYDEIYYFIDKLLSSSGGGVLINHKDCFQFIFEHLFNLILQSKQCTLELVNELIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IYNCKDCFEIFTKLSDSFIETIRATLYFENPAEQKQSDYETLNENCIFLMDLNLLDYF
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                           Agency: Deutsche Forschungsgemeinschaft (DFG).

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
                                                                                                                                                                                                                /organism-"Dictyostellum discoldeum'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref-"GI:21166071"
                                                                                                                                                          Location/Qualifiers
1. .129360
                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                           /strain="AX4"
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     Funding
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                                                                                                                                                             FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-MAY-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis of http://genome.imb-jena.de/dictyostelium/) and the Univerity Colonge, Institute for Biochemistry I (http://www.uni-koeln.de/dictyostelium/)
                        YSHSLLRDKFNKMKSSLWSICGKLAHEHKLPFKIKMKKWWKCCGHVTDELLIKEHDDY
NSIYNYINNESSSREQFLIFLNMIKHSWTTFTWETFIKCKISLENNMRNVTN"
1191 c 943 g 4950 t
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                                                                                                                                                                                                                                                                                                               NDKTSNDQANSSDSDCEPLPFGLKPSDLNRKVTEEDLERMIIELPGKLERKDMYLIWH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        598 AAAACTCACAACTTGATCAGATAAAATTTCATAAACACTTTTACGATGGATTCGTACGAT 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGACAATIGATTATAGATATATCCATTAATCCATGATATTATGATATAAATAGCTGTTA 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
1 (bases 1 to 12936)
Gloeckner,G., Eichlinger,L., Szafranski,K., Pachebat,J., Dear,P.,
Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K.,
Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (06-727-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 3 (bases 1 to 129360)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    658 CTATCTAATGACTTTTTTTTTTTTCTACCAGGTGGATGAAAGTTATAGTACTATTAGCCAG
                                                                                                                                                                                                                                                              AAAAGTATTAAAAGGAGCATAACGAGGCAACAAAAGTAATGAACACGGAGAAAAAGC
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                                                                                                                                                       Length 12029;
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                                                                                                                                                                                                           0; Mismatches 211; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Dictyostellum Genome Sequencing Consortium (bases 1 to 129360)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9275 TITIGCICTIATITATGGTTTTTCACATATCAGAAGTAT 9237
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                                                                                                                                                          Score 61.4; DB 3;
Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dictyostellum discoideum.
Dictyostellum discoideum.
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                                                                                                                                                       Query Match 5.6%;
Best Local Similarity 47.1%;
Matches 188; Conservative
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                                                                                                                                                     Query Match
Best Local Similarity
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CDS

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SADDLLIKKERERKEAIGSGSL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="movorrigagonkvigganokkiveseedialpeinpsvpoaio
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join(17001. 17789, 17899. 18159)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEKEEINESKNIFVNYDISIYCSTKEAIDNEPITKTLMRDGRDYTILWSRGYYLSGGS
KFGGTFLAYKGEPFLYPATFIVVIKRSNQTFQSLDIITTARLAVHVNKTTLIASLDEE
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PGCVHGGALASMFDDSMACCIRYFYNINFDDLNLQKOKOKOGOOGEGEOPGGNRNGI
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RAESTAIWIVVKIDTPISTTSSPPSFLSPLPSPTSNKLNENKLINENENNNNNNNN
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/note="ORF_ID:dd_03155"
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24154. .2652
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KINNKIWTENILIADINAFIEDCKMLLVLGREGAGGSTILRYTANOBESY ISVDGDVTY
ONIAASDWSKYRGETLYTGEDIHHPTLTVRETLDFTLKYLKTPGNRLPEESKRNFRTY
INELLVSWATGLVNGGDTWYGNEVRGLSGGERKRITTTEAMVSGSSITCMDCSTRGLD
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GALSGERRILQKHKSYALTKPGAYFVSGILIDIPFILVQVFHSFITYFWTGFSRADK
FFIFCFTLVGVBSASALFRGFANFTDFLTAQNLANFFYSTROFSYRADK
WRKWTYTINPLAYAFKSLMINFKGLDFSCLDSAIPPHFNNSTYSDMSHRICAVPGS
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FEDSGRQKMLINHKPKKMGVSIKNLTVVGQGADNSVIVDNSTPFKALGKLINPFNYFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 TTAACAGAAACTTCCAAATTTTTTTTTTTTGGAACAAGAAATAACAGATAGAAAACTA
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                                                                                                                         TSP418778 3364 bp RNA linear VRL 02-MAY-2002 Tomato spotted wilt virus NSs gene and N gene, genomic RNA, isolate
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NTVNTNGVKHQKKQHLKVLSPDQLHSIGSTMNRSDIKDFFQLQEKDIIPNDSYIALSVCS
NTVNTNGVKHQKKYIETCKNQALGKVNVLSPNRNVHEWLYSFKSFNQVESNNRFVNSLAV
SLLTSASHNIMPNSQAFVRSTSSHFKLSLMLRVPKVLRQVSIQKLFKVADDETNKT
FYLSTVCIPHHNSVPTALNISVICKHQLPIRKCKABSELSWYFSDLKEPYNIVHDSSY
PQRIVHALLETHTSFAQVLCNNLQEDVIIYTLINNYELTPGKLDLGERTLNYSBDICKR
KYFLSKTLECLPSNTQTMSYLDSIQIPSWKIDFARGGIKISPQPVSVAKSLLKLDLSG
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                                                                                         ATT-GATTATAGATATACCATTAATCCATGATATTTATGATATAAATAGCTGTTAAACT
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Submitted (05-NOV-2001) Adam G., Pflanzenschutz, Institut fuer
Angewandte Botanik, Ohnhorststrasse 18, 22609 Hamburg, GERMANY
Location/Qualifiers
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    /organism="Tomato spotted wilt virus"

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/db_xref="taxon:11613"
/country="Bulgaria"
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Tomato spotted wilt virus
Tomato spotted wilt virus
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/db_xref="GI:20429082"
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/protein_id="CAD11446.1"
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/db_xref="G1:20429083"
/translation="MSKVKLTKESIVALLTQGKDLEFEEDQNLVAFNFKTFCLENLDQ
IKKMSVISCLTFPRINGSINKVIKQBSPFTGKTITKRYSDSIRGATDMFRRLDSMIRV
RELVEETGNSENLNTIKSKIASHPLIQAYGLPLDTAKSVILAHIMGGSLPLIASVDSFE
MISVVLAIYQDANTKDGIDPKKYDTKEALGKVCTVLKSKAFEMNEDQVKKGKEYAAI
LSSSNPRAKGSIAMGHYSETLNKFYEMFGVKKQAKLTELA"
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94598, USA
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 171317)
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Homo saplens chromosome 5 clone CTD-231219, complete sequence.
ACO20941
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finishing Completed at Stanford Human Genome Center
Www.shgc.stanford.edu
Quality: Phrap Quality >-40 99.7% of Sequence;
Estimated Total Number of Errors is 2.7.
Location/Qualifiers
1. 171317
/organism="Homo sapiens"
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48.2%; Pred. No. 0.38;
ative 0; Mismatches 184;
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DOE Joint Genome Institute.
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Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, M., Nauyen, A., Nauyen, N., Nauyen, N., Nauyen, N., Nauyen, N., Okuchan, G., Oragunyen, N., Nickerson, E., Wockenker, S., Oguh, M., Okwuchu, G., Peters, L., Pickens, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Oride, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sutcon, A., Svatek, A., Tanerisa, A., Tamerisa, K., Stanley, H., Stonsey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Warfen, K., Wang, C., Walliams, G., Williams, G., Walliamson, A., Waerken, R., Washington, C., Watlington, S., Warren, R., Washington, C., Watlington, S., Weinstock, G. and Gibbs, R., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 60 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-UUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA

On Jul 9, 2002 this sequence version replaced gi:17941008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 233269)
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Consensus quality: 175720 bases at least Q40
Consensus quality: 180089 bases at least Q30
Consensus quality: 183792 bases at least Q30
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Contact: hgsc-help@bcm.tmc.edu
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AL732314 224635 bp DNA linear HTG 17-AUG-2002
Homo sapiens chromosome X clone RP13-465B17, *** SEQUENCING IN
PROGRESS ***, 8 unordered pieces.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 224635)
Whitehead, S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 21, 2002 this sequence version replaced gi:22204483.
--------------- Genome.Center
Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                    6 ACAAATTATTAATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTA
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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Chemistry: Dye-terminator; 100% of reads
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'S Lawson,D., Bowman,S. and Barrell,B.

Direct Submission

Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 187, UK
On to before May 14, 2001 this sequence version replaced
gi:2982540, gi:2982554, gi:2982564, gi:2894463, gi:2982566, gi:2982566, gi:2982566, gi:298256, gi:298256, gi:2884491, gi:2884589, gi:2884589, gi:2884589, gi:2884589, gi:2884589, gi:2884589, gi:2884589, gi:2884589, gi:2884589, gi:2884580, gi:2884589, gi:2884580, gi:2884589, gi:2884580, gi:2884
                                                                                                                                                       linear INV 22-MAY-2000
                                                                                 126 TGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTA 185
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

[ bases 1 to 253305]
Bowman, S., Lawson, D., Brown, D., Chillingworth, T.,
Churcher, C. M., Craig, A., Davies, R.M., Deviln, K., Feltwell, T.,
Gentles, S., Gwilliam, R., Hamlin, N., Harris, D., Holroyd, S.,
Moule, S., Mungall, K., Murphy, L., Oliver, K., Quail, M.A.,
Rajandream, M.-A., Rutter, S., Skelton, J., Squares, R., Squares, S.,
Bartell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 253305)
Oliver,K., Bowman,S., Harris,D., Lawson,D., Quail,M. and Barrell,B.
Unpublished
                                                                                                                                                                                                                                 TACGCGCTCAAAGTATGTTATCTAGTAGTGTAATTAATAATGCATGGTGCGATTCAGAA
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Consensus quality: 223253 bases at least 030
Consensus quality: 223562 bases at least 020
Insert size: 223555 bases at least 020
Insert size: 183401; 20.9% error; agarcse-fp
Quality coverage: 6.54x in 020 bases; sum-of-contigs Quality
coverage: 8.94x in 020 bases; agarcse-fp
                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown size soon as it is available and the accession number will be preserved.
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5.4%; Score 59.4; DB 2; Length 2;
Best Local Similarity 48.4%; Pred. No. 0.26;
Matches 165; Conservative 0; Mismatches 176; Indels
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/note="assembly_fragment:03847

fragment_chain:1"

180206. .187608

/note="assembly_fragment:01716"

187709. .191079

/note="assembly_fragment:02259"

/note="assembly_fragment:04008"

a 52985 c 53054 g 61479 t 70
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ORIGIN
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IFNKNYVLIERENEKECYLLSQKKOSTYVEDSVEPUNATOEEVFCOTARPLIPHVER
GINCTVFAYGATGSGKTYTMLDDKNONGIVOLSLLELFTIINEKKCRNIKVLMSFLEV
KNYTNTALLGKRENKTLEVORDASKVENLCEIEVANTSOAMLLINESVRNRSFEV
YNETIRDLLGKRENKTLEVORDASKVENCLEIEVANTSOAMLLINESVRNKMSPF
RANKVSSRSHAILQIYVYNEILDDNMNTISYRAKLCFVDLAGSERASATSNKGERFKE
SKYSSLANGLALANCINSLASNRNISKCYNYKRDSKTHLLKNSLEGNCLYVALANINP
SRTSFOESNNTLKYAFRYNKLACYOTNUNKESDIEKILKNSLCKEYDTLLGKY
TNLKEFFFIINTINOLYKROISCYKLIENISDNMSSMELKOOTTWYDOLYKKKSDEYR
KKVDSLKDLYOEKROISCYKLIENISTAVINSKOVNDNNKSLLEEMIFFKHNENK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        John (7801...7228, 8084...8234, 8392...8583)
/gene="PFC0870w, MAL3P7.3"
John (7801...7228, 8084...8234, 8392...8583)
/gene="PFC0870w, MAL3P7.3",
/grote="PFC0870w, MAL3P7.3",
/note="PFC0870w, MAL3P7.3"), putative elongation factor,
len: 181 aa; Similarity to P. falciparum elongation factor
1-beta, (AAF27524) (276 aa), fasta scores: opt: 366, E():
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation-"MRKTKNINDPFFINNYYYNKEENNPIIICSDEKERKTKIYSTNH
HTNNILNYNDHTLKLICNITENNKAILHSNKSNLQKNNILMPSYMQKKCTHIRETIKN
VYPNINGEPSTSVENITNGEHFINGQYDALKNMSLNNYDHQHNNIMNNISNKNKLFVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNENFLVNEKVYDKNIVLNGRYMYDENYVDRNIVLNGRYMYDENYMYDENVMYDENYWY UDENVW VDENVWYDENYWYDENYWYDENYWYDRNIVYYDK NV SVNEN I VYSEKHKYGLS
AEGRSESHNKNNKDDI EDNDKDT I KDI HNNNNSSDNNDDEY OSANSPVESDI VKKEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNNNNNSSSSSSSKVDGINILNNSNTNERLHTFSGVYSLNLNDEIKIEINKKDMEKN
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/translation="MGLFDKIRNIEKLNEAELKNIGNNDSSWHDQYRDSSYIYIGNLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRLTEGDIVIVFSQYGEPIDVNLVRDNETGKSKGYCFLSYADQRSTILAVDNFNGYKL
LERPLVVDHLLNYRLDKKYLKDADKNBYKPTGAEGGIGVINVVESEIKLSKVFDKIK
NKSNEEKKKKLLDBELWALNFEKSIKKDI ISPIGHDEKSRHNEGMKEEEEDDDDEDD
DDEDDDDDDSVDIKYKRHKERRKSLTTYKYDKKEKHRRKSDHRDKHRRRENHSRHREK
                                                                                                                                                                                                /note="PFC0860w (MAL3P7.1), Kinesin-related protein, len: 1200 aa; similarity: to kinesin-related protein.
D.melanogaster Kinesin-like protein 674 (TR:P91945) BLAST Score: 664, sum P(2) = 1.9e-67; 28% identity in 707 aa overlap, predicted using hexexon, Pfam: match to PP00225 kinesin, Kinesin motor domain Score 311.54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNNNNNNDDVIENMNEYPITSKNIYDSIYIPQINIKNIINSEEINNNNNNINDNNNH
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/gene="PFC0860w, MAL3P7.1"
/note="potential splice donor at 3' end of PFC0860w may indicate splicing"
4057. 4062
/note="potential splice donor at 3' end of PFC0860w may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIHLTSIDTISKIHARDLLKENKRKLENFQENIKHEHKDEVSLYVKKKKIKKKM
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/gene="PPC0865w, MAL3P7.2"
join(5457...5577,5689...5787,5923...6077,6189...6743)
/gene="PPC0865w, MAL3P7.2"
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/protein_id="CAB39067.1"
/db_xref="GI:4494008"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="kinesin-related protein"
/protein_id="CAB39023.1"
/db_xref="GI:4493964"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKDKKSHKRRHKHSYDKYSSRSRSYSTSSTDR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref-"SPTREMBL:097277"
                                                                                   /gene="PFC0860w, MAL3P7.1"
                                                                                                                                                                   MAL3P7.1"
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Join(5457. .5577,5
clone-"MAL3P7"
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                                         .4060
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INNNINNNINNNINNOHRNNGCYLIIONVNKFYGKKHALKDVSLTLRSNRIFVLLGE
ROSGRETLINIITKMISKOSOBINFKRNSYKNKKDIYMDVRNRRRRGLGRICSNGY
IKEEVAMRIFKRNGOTNNYDNNSNNNNNDHNDHISNNSGINSSFNNNHHNKNI
KNDLEISYCSONVILYENLIFYETIKIFLLYYNKNVDKYLNKKRTLKIMNDLDLVQYL
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/translation="MKDFLSYAENNDLNIFKLYNSEEDCLKNLKYAIELKSEDFKNVN
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MLNTKYRGKSKSITNDKRKKSQQKTYEYGNINYDMSEKYPTHQLKDNSNDFMLEGSDE
DDTCYELDTLHKKQVNSQMCLRIEKIRNDRRESNGHPYDIPMIPLRHINNINNNINNN
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YLSQEKIMSALNKKGVIKSPRKVANNYVDGYNVGRISSHESSINDKKKDNNDNNDDD
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DIKYLI EIDPLFFLF FQNFKY FNELNNLLLMKNNHMQP I SYNFAYLKDILVRGNENKN
I INSTNHDDNPYDI NMYNNHNKYGKY KNNNNNNSFYNMRDDTELTDI EENI SSKKKKN
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FHEHFMRDFYINIYVFLSIVIFFCVFFERFKNBIENRKIFENPHVHQYIHYFQILLLE
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YFFNDININLKQNFINFNTVDDLSFNIYFNEMYYFSFFIVLEYQFNSFILNYNADILK
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LLFTIICMQFSNNSSINYIATFLLFFLFSSFRLIIHSGASNILTFFVLLIPHSSFCLS
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YSTISSNHLKQSTINY FILYKNEMNNETLGYNKYNLNDDNIKKNLNNSYDKILKKLE
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ILDGSTYDNIKVVEDVKGNCDMNTLLYDKENKYNYLIKDIDNKNIREECNANFRLSKN
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NQNEHISEKIQKMNERDYKIELIPTMSIYEHFKIILTFKNIELTNVELKYIINLLMLI
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Incher splicing of PFC0870w*

further splicing of PFC0870w*

Join(1431. .20416,20578. .20690)

/gene="PFC0875w, MAL3P7.4" .20690)

Join(14431. .20416,20578. .20690)

/gene="PFC0875w, MAL3P7.4", hypothetical protein, len:
/note="PFC0875w (MAL3P7.4), hypothetical protein, len:
3032 aa, revised: added 3' exon, possibly spliced at 5'
1.1e-15, 53.2% identity in 141 aa overlap, revised:
shortened exon 2, Pfam: match to PF00736 EF1BD, EF-1
guanine nucleotide exchange domain Score 61.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8235. .8240
/gene="PFCO870w, MAL3P7.3"
/note="revised splice donor sequence for exon 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product-"hypothetical protein, PFC0875w"
/protein_id="CAB39024.2"
/db_xref="GI:8052275"
                                                                                                                                                                            /product="putative elongation factor"
                                                                                                                                                                                                            /protein_id="CAB39068.2"
/db_xref="GI:8052274"
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Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Moner, G., Miner, G., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Maser, M., Neal, D., Newtson, J., Nouven, A., Nguyen, N., Oviedo, M., Nguyen, N., Oviedo, R., Pave, N., Pance, A., Payton, B., Peery, J., Okwonn, G., Peters, L., Pickens, R., Prinus, E., Pu, L., L., Quiles, M., Ren, Y., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutcon, R., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, S., Wanch, M., Varquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Walllams, G., Walliamson, A., Washington, C., Watlington, S., Warten, R., Washington, C., Watlington, S., Walliamson, A., Washington, S., Warten, R., Washington, S., Warter, R., Washington, S., Warter, R., Washington, S., Warter, R., Washington, S., Warter, S., Washington, S., Washington, S., Warter, S., Washington, S., Warter, S., Washington, S., Warter, S., Washington, S., Warter, S., Washington, S., Washington, S., Warter, S., Washington, S., Warter, S., Washington, S., Warter, S., Washington, S., Warter, S., Washington, S., Washington, S., Warter, S., Washington, S., Washing

2 (bases 1 to 165669)
Worley.K.C.
Direct Submission
Submitted (07-MAR-2002) Human Genome Sequencing Center, Department
Baylor Plaza, Houston, Tx 77030, USA
(bases 1 to 165669)

AUTHORS TITLE JOURNAL

TITLE JOURNAL REFERENCE

Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 12, 2002 this Sequence Version replaced gi:20467600.

COMMENT

Direct Submission Worley, K.C.

REFERENCE AUTHORS JOURNAL TITLE

Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu

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AC114238.6 GI:21738343 HTG; HTGS_PHASE1. LOCUS DEFINITION ORGANISM ACCESSION RESULT 11 VERSION KEYWORDS SOURCE REFERENCE AUTHORS AC114238

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). Graft This is a "working draft sequence. It currently consists of 49 contigs. The true order of the pieces arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will Center project name: GQXB
Center clone name: CH230-336N7
Center clone name: CH230-336N7
Sequencing vector: plasmid.
Segmenting vector: plasmid.
Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 138160 bases at least Q40
Consensus quality: 133217 bases at least Q20
Consensus quality: 136246 bases at least Q20 1074: contig of 1074 bp in length 1174: gap of unknown length 2179: contig of 1005 bp in length 2279: gap of unknown length 3300: contig of 1021 bp in length 3400: gap of unknown length 4592: contig of 1192 bp in length 6519: contig of 1527 bp in length 6319: gap of unknown length 6319: gap of unknown length 7439: contig of 1120 bp in length 6319: gap of unknown length 7539: gap of unknown length 7539: gap of unknown length 7539: gap of unknown length bp in length length unknown οŧ contig gap of 1175 2180 2280 2280 3301 3401 4593 4693 6220 6320 7740 7540 9319 1075

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Ruzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, H.C., Burrell, R., Byrd, N. C., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Carter, Davis, C., Davy-Carroll, R., Chacko, J., Chavez, D., Carchard, C.D., Cox, C., Coyle, M. D., Dathorne, S.R., David, R., Delandy, R.R., Delgado, O., Davy-Carroll, R., Dinh, H. H., Davis, C., Davy-Carroll, R., Dinh, H. H., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Galbis, T., Ferraguto, D., Flagey, N., Fostd, J., Harlis, R., Harlis, R., Hartis, C., Harris, K., Hatt, M., Hatlak, P., Haees, A., Hernandez, J., Harris, C., Harris, K., Hatt, M., Hallak, P., Haees, A., Hennandez, J., Hodward, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. E., Karlsoon, E., Kally, S., Khan, U., King, L., Korvah, J., Kovar, C., Liu, J., Li, Z., Lichtaria, M., Liu, Z., Lichtaria, P., Martin, R., Lucier, R., Luna, R., Martinez, E., Lucier, R., Luna, R., Martinez, E., Rattus norvegicus clone CH230-336N7, *** SEQUENCING IN PROGRESS
AC114238 Norway rat. Buttus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalía; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;

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Young,J., Rowen,L., Madan,A., Qin,S., Abbasi,N., Dors,M.,
Dickhoff,R., James,R., Loretz,C., Lasky,S., Madan,A., Prescott,S.,
Ratcliffe,A., Shaffer,T. and Hood,L.
Direct Submission
Submitted (30-MAR-1999) Multimegabase Sequencing Center, University
of Mashington, PO BOX 357730, Seattle, WA 98195, USA
B 3 (bases I to 192389)
S Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B.,
Bloom,S., Dors,M., Dickhoff,R., Harrison,G., James,R., Lasky,S.,
Madan,A., Ratcliffe,A., Shaffer,T. and Hood,L.
Direct Submission
Submitted (25-AUG-1999) Multimegabase Sequencing Center, University
of Washington, PO BOX 357730, Seattle, WA 98195, USA
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Homo sapiens chromosome 14 clone BAC 507E23 map 14q24.3, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rowen, L., Madan, A., Oln, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Harrison, G., James, R., Lasky, S., Madan, A., Ratcliffe, A., Shaffer, T. and Hood, L. Sequencing of human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 AAGAAATAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 AAATTTTAAAAAATTATATAAAGCCTATACGCGCTCAAAGTATGTTATCTAGTAGGTGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 TTAATAATGCATGCGGATT -- CAGAATTGGGACAACAATGAAAACGGAATTAAAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.3%; Score 58.6; DB 2; Length 165669; Best Local Similarity 53.8%; Pred. No. 0.38; Matches 142; Conservative 0; Mismatches 120; Indels 2;
                   contig of 7534 bp in length gap of unknown length gap of unknown length gap of unknown length contig of 9957 bp in length gap of unknown length gap of unknown length gap of 16404 bp in length.
                                                                                                                                                                                                                                                                                                                                                        7115 others
length
                                                                                                                                                                                                                                    1.165669
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a 31280 c 30162 g 48184 t
  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 TAACTTTAAAATAAATATT 301
                                                                                                                                                                                                                   Location/Qualifiers
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AC007182.3 GI:5708446
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                                                                                                                              149165:
                                                  132157:
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Gaps

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97 AACAAGAAATAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 TAATTAATAATGCATGGTGCGATTCAGAATTGGGACAACAAAAAAAGGAATTAAAATA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG 18-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (18-MAY-2002) Genome Analysis, Institute of Molecular
Buctechnology, Beutenberstr. 11, Jena 07745, Germany
CDS predictions from GeneID may contain errors. Further Information
is available from IMB Jena, Department of Genome Analysis
and the Univerity Colonge, Institute for Blochemistry I
(http://www.uni-koeln.de/dictyostelium/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Mycecozoa; Dictyostellida; Dictyostellum.

1 (bases 1 to 115489)
Gloeckner, G., Elchinger, L., Szafranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dictyostellum discoideum chromosome 2 map 3426827-3542314 strain ARX4, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                        GHFLSELFVYGTAAPTIGVLAPLMVASFSILGMLVGLRYLEVEPVSROKKRN"
163815. .164050
//note="low quality data"
173850. .173930
//note="low quality data"
191730. .191800 quality data"
52511 a 41950 c 43606 g 54322 t
                                                                                                                                                                                                                                                                                                                                                                                                          157 AGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTCAAAGTATGTTATCTAGTAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277 ITAACTITTAAAATAAAATAAAATITGAGTAAATGTGTITTCTGACTATTGAGGGGGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 192389;
                                                                                                                                                                                                                                                                                                ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agency: Deutsche Forschungsgemeinschaft (DFG).
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Dictyostelium Genome Sequencing Consortium
                                                                                                                                                                                                                                           Score 58.6; DB 9;
Pred. No. 0.37;
0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115489 bp
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HTG: HTGS_PHASE2.
Dictyostelium discoideum.
Dictyostelium discoideum
                                                                                                                                                                                                                                           Query Match 5.3%;
Best Local Similarity 52.7%;
Matches 127; Conservative
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                                                   unsure
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AC117072/c
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TITLE
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IFTLSQGQIIDNYGTWGFWTGYLPLGFERAVELTYPESEGISSGLINISAQVFG
EEESNTSKVPTAVSEDHL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The
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and 368K8, Accession AC009399."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="maqydsglelswgslfaaaaaaataylgarspamgntlosfrdh
PFLYEKLYTGRPNLVNGLQARTFGIWTLLSSVIRCLCAIDIHNKTLYHTTLWTFLLAL
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/note="Intron-exon boundaries were defined partly by Genscan and partly by ESTS. See 179253 and AA305338 closest BLASTX hit is to AF118637, 'C receptor.'"
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62125. .62265

/note="low quality data"

90750. .90850

/note="low quality data"

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Location/Qualifiers
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CDS

CDS

CDS

CDS

FEATURES

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RNQEDPLYTLAGHODTITSTSYSKDGAYLLSNSMDNSCKIMDIRPYAPPNRIKTENG
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NEPITASCSSRYIYLGEIKP"
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13514. 113889)
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AGILLYIGFSLMIKDFPEDMEELCRGKKYEYFLRAGLFIGLWVGAAMMAFIGKYL"
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/translation="Meeoillooperscore"
/translation=
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IGIGVVLSCAFIHMLLPAVISLTSECLPESWHEGYEAYPYLFALLAGIVMQFIDFVVL
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GDDKDQLFVIIDFSEDILKLVYEERKEKEKEKEKEKEKEESQSFIGKYWFYLLPLFII
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GYLEESRKQRKALIANGEKCTKDLKTAESNESKAKONYEKLKRKQEEANEDLSKQPPG
AKEQKARKTLESATKAADKGDNEYRESVKCLQONQQKFYHEEMPRILDDLQRFEVERI
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/db_xref="G1:20976564"
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/note="ORF_ID:dd_01647"
/codon_start=1
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comptlement(join(21183. .21470,21613. .21894))
//cofon_start=1
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/db_xref-"GI:20976563"
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/note="ORF_ID:dd_01650"
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/db_xref="G1:20976602"
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/note="ORF_ID:dd_01648"
/codon_start=1
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20947. .2096
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STREFFEFFYTIITYTLFTTYSSDSFWYLITATAFEMBLSGIVGDIVATTFSIFF
NHLMTSIFLYMLFILTTSGIFLSSKNDKLNWFTGKRMYFEISSLYGVYRSPFRSPIF
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ELKSPKRSKKKKKKKTITNIHSRLSNSLSDLPULSQINNNNNSTSLSYRYEIEINNNNK
ELVLTPRSKKKKREKTENENEKKILIENSNLIIEGFREKFIKYNVKYSKNLNMLSTYL
KECDQEFWNKDLVSHPWQLAILLEKNNNINMINMGAISIONSSCHFLLPFFIN
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EDLDAKNIKTKSLNYSQERILKKYKFR TEKDEWENKERKEIFTUNDLHLEEDSQCEI
SRIHFFWILLTSFTRQOKELSTIVYTWSRCIYRQNRITHFEWFLLILCWFLAPPKFLY
CKFKIFLKNRKQNKKLKKQRKKQKGEDEYEEDEEDKEEEVENNYLFNFKNRKNEIKLK
KTNRNYLISTIFCKNKFTITKFTILLSFIGTVFTITRYRILLFYFTLY
ASPENGASGFYCCMRFFGTLLGYFSAVLYGYLESTADSGFYGLAYTALTFTLYFSIH
FFVRGKPIGSFGCNFFILLSYSATITFFEYTQDHALITTLLRAFHISLAVFVIHLSSILI
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/db_xref="GI:20976560"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISPSTSSTSLANSPTPSPSTLPNSNSQQQQQQQQQTWKSCCGNSRCMLCGNGTPRC
LCMNHPSWTLILRVVFFSLSQLYPDKEFFNLKKEVYVYLNDHWEILSPNQKQSHNWRR
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VENBIKKYYENNNEKNIDYLNSLLAVQVDITNEESVENGVKETVNKFGHFDVVINNAG
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GLTLSLEQELAPFNIKVVLLSPGGFRTITTNKEKFKLVENPIPEYYPNSTPQNSLEAF
IGLMNTSNGDPNKFANAILKLDLIHQQGNKLPSNIFFGSDALEGSSHFFKSLIDESNQ
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PKEIFQETWRPIFLEIRSLITNQRSLMFNSRPELLFNKQKYKDLKSLLNNISSEYMVL
VGSEFIIDNCQEDGNDSYHNHHHHHHHNSKNYDQTNFLLDVKSLLLPKFNYLIKELDE
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FCVHQLGCLIYTFDLFINLMSNITKYIMSITKTILIERKDSNYLYNNNLNSLDNLVTM
SNSSINSSKNINNNNNSTCIDSSTFTSSSSDNNSEDLIIPINRSQFIRHTSIGGTEYN
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as soon as it is available and be preserved.
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/note="ORF_ID:dd_03233"
/codon_start=1
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/protein_id="AAM33147.1"
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1001. .2764
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     * by the finished sequence as
* the accession number will be
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="2"
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/note-"ORF_ID:dd_01651"

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/codon_start=1
Funding
                        Agency
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              /product="Sequence 3 from Patent W00075321. 6/101"
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LGFWHNMLIRPANREELRNFGERDYTTYNAGGPFANRYTKGMSSSSTAIDFARKEMVI
LGTQYAGEMKKGILITIMMYLAPKMGYLPLHSSCNQARNNGDTTLFFGLSGTGKTTLSA
LGTQYAGEMKKGILITIMMYLAPKMGYLPLHSSCNQARNNGDTTLFFGLSGTGKTTLSA
DINNELIGDDEHVWTDTGCFNIEGGGYAKCIDLSREFEBEIFDATRGAVLENVYNE
NOWWHYFLGGFTARVAGTENGYTERTFSSCYGEPFIVHHPTKTAEMLASOLHKHS
ANDWHYGGSHGVGSRIKLAYTRAIIDAHSGELRIPTKMDYGGFOVPNSCP
JOINC28969. 29084,29176. 29317,29453. 30610)
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC115575 27291 bp DNA linear HTG 21-MAR-2002 Dictyostelium discoideum chromosome 2 map 1180800-1208089 strain AX4, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
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1 (Dases 1 to 2729)
610eckner,G., Eichlinger,L., Szafranski,K., Pachebat,J., Dear,P.,
Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K.,
Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Gaps
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Best Local Similarity
Matches 155; Conserv
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AC115575/c
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JOURNAL
REMARK
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AUTHORS
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/LTAIS.14 tion="WINYLVILLI-FFIVI IGCVVSLKSPIKSKIDVPRLNNQQVRYPSD ETWSEVDTFLEEAIENGTFPGCVALVCNAGKGYLIAAAKGSFTYGIGTPINDFWYPPB ETWSEVDTFLEEAIENGTFPGCVALVCNAGKGYLIAAAKGSFTYGIGTPINDFWYPPB LSTLEDMASCSKVTACTTSVAQFYQRGELNLDSPITDFLGLEFGVNGKSGISVRNCLL HNSGFYPDPRPWETCOSOIYQSTLNOSILMPIGSTVYS DLNFWTLMYVVGNAGFNYTTADQLTPGCDNGAPENAQCYYEAYVRHYPTNAUNTWYTATVGVYSDGNAZALGGISGHAGVFSNVEBMYF MYSLMTATQGVYSDGNAZALGGISGHAGVFSNVEBMYF MYSLMTATATGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSBANTATTGGYSB
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KOLEPLGINKIEITDKYTHINNSFPCLNKTNNGGEKCKQLISTLVNKNNKNYKLISKI
IYPFOENVGKYFDNNMLNYKSYLOBEKLIALGTINNNEMVVSNAINIIDDPIEKCI
PPKSIKCNSGSIITNSRDFKRCLINNSTCTPLAFNGNTTVVIPIYPTCPKGYYLFFFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POYSAOKVATRENSET ATALLS IT ITS ASSELLITERS TRUDBENING TRAPC
KVVRYKSLEPLGNPASATUKYY IFGENGVRCYTFESEASELITES TORNEFFERAKD.
KVVRYKSLEPLGNPASATUKYY IFGENGVRCYTFPCASTDAVLLNI RRKQTVSDLLMP
KRNVGKYFDSAWLGSKTVRSDDYGLIGOGFFSSGK.TISNAFIHLPDPIGKCDSLPL
LKCFGGSTATTYSRNENRCLASPTCTQSSFCTLGMPLCPAGYRLDQFRATEANGCPKYY
CDPTFYCKTH*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MIKLFCISAILFIFFIFSLGESTLIRPNFYRIDWENINCIRAPC"
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TDFLVTRVYKSLPLGNKQTSTDKYYMFGDNGTRCKTSFCPNTVAALLAVHSQBIINTI
SQPYEKNVGFLDSVWLSSKNIRSDDFGLIGQGTIKNGVISISNSFIYLPDPPIKCPEL
PLLKCVEGNSMTYSRDENRCLVSPRCTKFGVCTLSIPLCNKGYRLVSFPSTELNGCPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MIKNYKLLLFTTFTLFFITFVSGSSILKANFYYKVDWENVQCFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(163. 380,1237. 2062,2157. 2468))
/note="ORF_ID:dd_00011"
/codon_start=1
                           * NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* Ty he finished sequence as soon as it is available and

* the accession number with the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="Hypothetical protein yfeW precursor"
/protein.id="AAL9218",1"
|D_xref="G1:19569868"
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/note="ORF_ID:dd_00013"
/codon_start=1
Deutsche Forschungsgemeinschaft (DFG).
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                                                                                                                                                                                                                                                                                                    1. .27291
/organism="Dictyostelium discoideum"
                                                                                                                                                                                             the accession number will be preserved Location/Qualifiers
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/db_xref="GI:19569870"
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/db_xref="GI:19569871"
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/db_xref="G1:19569872"
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/db_xref="taxon:44689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="1180800-1208089"
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ASKKLMISSVOTMOYAEELYTKGLISERPRETDSFQAGGINKRIYDFITRRIACCSEESV
FANTTVTDIQGERFSETGTWAKLISEVPEDKRANTNITRGRANGERFSTELTRKRIUGV
KGTYVAPHYTTEAELLTAMDNNKIGTDATMATHIOTOGREFVKRIUGV
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YESNYPLPDSNWLFQCSNDNTRACITLSIGSTGYDLYSSSFVRLPDPISONCPALPL
LKCQGGHYTVYERDSNRCLTNPQCSNDNDTRACILSIPTCSTGYDLYSTSISTCPAY
NCDAXFLTKTY"
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DEDRIFYNTALINFYSTSLSINNNNNEFGSSPSLALTRYVLINFDDGYLDDNSF
KLIOKSKINNTTTRENSKOLEIKOAKEFIDNIKKONTCONNNNI I IFSSKRISL
SCLKLLODNNIKTIFNLDNNOLFNIOQYTNSSYILNSITSNITKNSSSSGSSIFGNCN
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INGGSSNEIKLSVEIKEKIKSSPSTEKTKAPSFIFI IEBVQKSKNDSISTILSILVKKKKF
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                                                                                                                                                                                                                                             /translation="MKQLEFTAVHAIFKILSTSLGPKGLDKVIVNIOKSKTFEKNESQ
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KLLIRNYHPNLIIKAFTIAYEQSKLLLNSNSIELSITNDLLSNNFNIINNNNSGSEY
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TKTOSOTGTOSQQARKPASKPIEFLNKFEKSLVITENENASLIPPNLTFDKNVDNEKT
KIDKOPQKSTTTNKTISKPKKTITTODLKVP EKKETKINSDDEEDDDOSDLNYYS
EDDTLLGDEQDDAPWYLNEDEDENDNINEDEEDENKSDKSEDEFSLFRPTOMSSKRV
EELFKPHISNYHWYSTLSQFTTKHTNNFLORNOINTESTILEONLOIKSNLHSQLSLY
VQSVIDQLGFKITTAKEKVTILLDFFKFDKPVPSLRRNHWKILSSIDEELIKDIKDIN
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IDFPDLPKNGDISQLVTSMGVPQNCPICQYQVLSVRNPINDKSYTICPKCRNSPPDPI
MRKPPHCFQCTFNCNLAFROKQQQQQQQQQQQTNYNRNNNNNTNSARPITTRTRT
mmontenger a chinibanina barbanningtet
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SLIEDETTENELRSHYYNLFQPDHFKDVVAERSASGKCGYPCCSKPLGVKKLNQKYFI
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17950. .18303))
/note="ORF_ID:dd_00010"
complement(join(8905. .9372,9507. .9941,10051. .10237, 10316. .10739,10891. .11140))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-"SIMILAR TO HYPOTHETICAL 26.2 KD PROTEIN"
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/db_xref-"GI:19569876"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLKMIDTVSMIIKIDQLIKN"
join(12238. 12622,12711. 13189)
/note="ORF_ID:dd_00008"
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/db_xref="GI:19569873"
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/product="hypothetical protein"
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Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.
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KRVNDLLLEIKYSSPEQKROLAQSKLFQDVLKDFDHLIVYFDQPPPQIKTIYVPVQP
IPQPRYVNNFPTIPTMPSFSPPDYNSSMFNNGNKPPTITTTTSNQPFQNLDPFNNTA
                                                                                                                      ITPFSTNPFFVDQNVSQGLMKTRPEEESARKLKELFPNTSDEVVRYVLLSTDNNMSLA
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Plasmodium falciparum.
Plasmodium falciparum.
Plasmodium falciparum.
Plasmodium falciparum.
I bases 1 to 169546)
Hyman, R.W., Fung, E.L., Qin, F., Rowley, D., Mao, J., Tamaki, T., Kurdi, O.B., Conway, A.B. and Davis, R.W.
Dlasmodium falciparum 3D7 chromosome 12
                                                                                                                                             IONLLDITIKVENSKNASN"

join(21265. 21568,21981. .22138,22341. .22457)

/note="ORF_ID:dd_00014"

/codon_start=1
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                                                                                                                                                                                                                                                                 mitochondrial precursor"
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us-09-502-426b-1_copy_2102_3202.rge

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13340 TTATGAAGAATTAAATATGTAACTATATAATACTATATAAGAATATATAAATATATA 13281
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                    Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W. Direct Submission Submitted (19-FBB-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
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(bases 1 to 169546)
nan,R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
                                                                                                       on Aug 12, 2000 this sequence version replaced gi:8810447.

* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces arbitrary Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
5.2%; Score 57.8; DB 2; Length 169546;
Best Local Similarity 49.9%; Pred. No. 0.52;
Matches 173; Conservative 0; Mismatches 172; Indels 2;
                                                                                                                                                                                                                                                           3467 23466: contig of 23466 bp in length
3467 23666: gap of unknown length
3667 169546: contig of 145880 bp in length.
Location/Qualifiers
/organism="Plasmodium falciparum"
/db_xxef="taxon:5833"
/clone="pryAC293"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 others
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a 15381 c 15705 g 68389 t
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 REFERENCE
AUTHORS
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JOURNAL
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3203..3423
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3424..3503
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AAS61424
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3829..3913
/*tag= g
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3504..3828
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9837.455 Million cell updates/sec
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT
                             5.1.6
Compugen Ltd.
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                             GenCore version
Copyright (c) 1993 - 2003
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22alpha-hydroxylation steps in brassinosteroid biosynthesis. The DWF4 polynucleotide is used for altering the phenotype of a plant. DWF4 plants display a dramatic reduction in the length of different organs, and this size reduction is attributable to a defect in cell elongation. The DWF4 polynucleotides and polypeptides can be used in diagnostic assays and to generate antibodies, which can be used to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated \text{dwf4} polynucleotide useful for altering the phenotype of plants, for diagnostic assays and in the production of antibodies -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention may be described as cytostatic. The object of the invention is signalling, as well as oligonucleotides and/or PNA-oligomers for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumnours and cancer. The sequences given in records ABL70111-ABL70626 represent chemically pre-treated with cell signalling.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signalling
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                                                                 Chemically treated cell signalling DNA sequence complementary to#140.
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                                                                                                                                  Cell signalling; cytosine methylation; cell signalling disease;
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                                                                                                                                                                 cancer; tumour; cytostatic; ds
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01-JUL-2002 (first entry)
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nes 164; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EPIG-) EPIGENOMICS AG.
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Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; ososphageal cancer; ds; tumour; immunostimulant; cardiant; antlinflammatory; coagulant; antlasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to 224 nucleic acid sequences comprising at least 18 bases of a chemically pretreated gene associated with gene regulation selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the 5-position to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer. Werner syndrome, asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preeclampsia, graft versus host disease. The present sequence is a sequence included in the sequence data for this specification and is associated with the human gene regulation associated genes.
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                                                                                                                                                                                                                                                                  Human gene regulation-associated gene oligonucleotide #297
                       Sequence 6107 BP; 1604 A; 136 C; 1251 G; 3116 T; 0 other;
326 GAGGGCCAAAAAAAAAGACAATGCCAAAAGTCTACGGGTTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID No 304; 26pp; English.
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2000DE-1019173.
2000DE-1032529.
                                                                                                                           1342/c
AAS61342 standard; DNA; 6107
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30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                       29-JAN-2002
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                                                                                                                                                                                   AAS61342;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4531 TAAAACTCATAATTTAAAAAAAAAAAAACGAAAACTACTTATTATTATCACTTTTCTTTTCC 4472
                                                                                                                                                                                                          145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or displayments. Also disclosed are obligonucleotides and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonuclectide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction
                                                                                                                                                  4771 CAAAAAAATAAAATAAAATATAATAATAAAAAAATCTAAAAATACATAAAATATCTT
                                                                                                    26 CAATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTAACAGAAACTTCCAAATTTTT
                                                                                                                                                                                                     TTTTTTTATGGAACAAGAAATAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGT
                                                                                                                                                                                                                                                   4711 TTAAATAAAAAACTAAAAAAAACCACTAAAAATTTATAATTACAAAAATCAAAAATTT
                                                                                                                                                                                                                                                                                                    AATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTCAAAGTATGTTA
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     Length 6107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 GAGGGCCAAAAAAAAGACAATGCCAAAAGTCTACGGGTTTGAC 368
     DB 24;
     Score 56.6; DB;
Pred. No. 0.044;
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     5.18;
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01-SEP-2000; 2000DE-1043826.
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                                                     Matches 164; Conservative
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Query Match
Best Local Similarity
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4771 CAAAAAAATAAAATAAAATATAATAATAAAAAAATCTAAAAATACATAAAATTCCTT 4712
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   The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK3155 represent chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent. Office.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 AATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTCAAAGTATGTTA
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epigenetic parameters of genes associated with signal transduction.
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Pred. No. 0.044;
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98US-0085537.
98US-0085696.
98US-0105234.
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15-MAY-1998;
21-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        765 GNNTTAAGGANAATANATNAATAGATANNTNAAATAAATTATAATATATAAAAATANNA 824
                                                            Labat I;
                                                                                         Polynucleotide library used to determine cancerous states of mammalian
                                        J, Innis MA, Garcia PD, Sudduth-Klinger J;
Randazzo F, Kennedy GC, Pot D, Kassam A;
Crkvenjakov R, Dickson M, Drmanac S, Labat
Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                  1 AATCTACAAATTATTAATATTTAGTCAATAACAATGCATAGAAAAGTTCCAAAAAAATTT
                                                                                                                                                                                                                                                                                                                                                        585 atatanaggaaaagtaaattaatngatattaaagaanaaagaaaaanaaatatanan
                                                                                                                                                                                                                                                                                                                                                                             121 tatitigtigtggaatggaagtagtaatatacattaagcaaatittaaaaaattataa
                                                                                                                                                                                                                                                                                                                                                                                         181 GCCIATACGCGCTCA----AAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                         236 cgaitcagaaitgggacaacaatgaaaacggaaitaaaataacttiaaaataa
                                                                                                                                                                                                                                                                                                          5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        825 AATAATGAGNTGANNGATTATANNAANNTATANNGTATNTAATATAAA 874
                                                                                                                                                                                                                                                                                    4.9%; Score 54.2; DB 21; Length 875;
42.6%; Pred. No. 0.1;
itive 0; Mismatches 196; Indels 5
                                                                                                                                                                                                                                                       negative breast cancer, lung cancer, and colon cancer
                                                                                                                                                                                                                                                                   Sequence 875 BP; 421 A; 10 C; 78 G; 198 T; 168 other;
                                                                                                               Claim 1; Pagė 720; 1097pp; English.
  98US-0105877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA; 6113
                                                                                                                                                                                                                                                                                          Best Local Similarity 42.6
Matches 149, Conservative
                                       Escobedo
                                                           Leshkowitz D, Kita D,
                                              Giese K,
Drmanac R,
               (CHIR ) CHIRON CORP.
                                                                          WPI; 2000-126369/11.
                        HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL32803 standard;
27-OCT-1998;
                                     Williams LT,
Reinhard C,
                                                     Lamson G,
                       (HYSE-)
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ABL32803/c
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26-MAR-2002 (first entry)

ABL32803;

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences and be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and necular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 TACGCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATT 240
                                               Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
4.9%; Score 54.2; DB 24; Length 6113;
Best Local Similarity 51.9%; Pred. No. 0.13;
Matches 122; Conservative 0; Mismatches 113; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6113 BP; 1694 A; 157 C; 1445 G; 2817 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 776; 32pp + Sequence Listing; German.
Human immune system associated gene SEQ ID NO: 776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS
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                                                                                                                                                                                                                                                                                                                                                        WO200200928-A2.
                                                                                                                                                                                                                                                                                                      Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                03-JAN-2002
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ABQ67094 standard; DNA; 83391 BP

ABQ67094 RESULT

ABQ67094;

8117 TTTTTTTTTTTTA 8101

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 AGAAACTICCAAATTITITITITITATGGAACAAGA-AATAACAGATAGAAAACTATTIT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8297 AAATTAATAAAAATTAAAAAACAATAATTAAATAAATTTAACATAATTAACAAAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACGCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 GTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAAAACTAAAAAAAAATTACTTACTATAATTAATTATAACAAAAACTAACAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                  antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirhematic; antiarthritic; antidiabetic; antipsortatic; antiariamatory; cancer; eye disease; arteriosclerosis; anacute myeloid leukaemia; Alzhelmer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                      Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53.8; DB 24; Length 37973;
Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37973 BP; 10756 A; 620 C; 8310 G; 18287 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 2170; 32pp + Sequence Listing; German.
                                   Human immune system associated gene SEQ ID NO: 2170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.9%;
                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                 02-JUL-2001; 2001WO-EP07537
 26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytosine methylation
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                                                                                                                                                                                                                                                               WO200200928-A2
                                                                                                                                                                                                                              Homo saptens
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75008 AGTAG-AGAAATGATTACGTAAATAATAGTATATTATATATAATAGAATAGTATGAAG 75066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bases of chemically pretreated DNA of angiogenesis associated genes (II) having sequences (ABQ66971-ABQ67178) or their complements. (I), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in angiogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, necvascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation, psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printer specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                      Human; anglogenesis; methylation; eye disease; glaucoma; tumour;
inflammation; rheumatotid arthritis; diabetic retinopathy; antiulcerds;
macular degeneration; inflammatoy bowel disease; Crohn's disease;
antirheumatic; antiarthritis; antidiabetic; antipsoriatis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a nucleic acid (I) comprising a segment of 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 TGTGGAATGGAAGTAGTAATATATATAAGCAAATTTTAAAAAATTATATAAGCCTATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 GAAACTTCCAAATTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAACTATTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           angiogenesis-associated genes, useful for determining methylation status, e.g. in diagnosis or treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 83391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 83391 BP; 24547 A; 665 C; 16953 G; 41209 T; 17 other;
                                                                                Human anglogenesis associated polynucleotide SEQ ID NO 124.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid fragments from chemically treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 53.8; DB 24;
Pred. No. 0.23;
0; Mismatches 167;
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Best Local Similarity 49.5%;
Matches 165; Conservative
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                                          (first entry)
                                                                                                                                                                                                      antiarteriosclerotic; ds
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                                                                                                                                                                                                                                                                                     WO200246454-A2
                                                                                                                                                                                                                                                 Homo sapiens.
                                        28-AUG-2002
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29

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6807 ICTTAAACAATAATAAAAACATAAATATTCATCAAAATACTCTATAAACCTTTTCATTTA 6748

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88 ITITTATGGAACAAGAAATAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAA 147

6747 ACTAAATAATCTAATTTTAAAAACCCTAAAATCATAAACATATTCTATATTTTCA 6688

148 TATACATTAAGCAAATTTTAAAAATTATATAAGCCTATACGCGCTCAAAGTATGTTATC

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308
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189 GCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTG
                                                            including eye diseases such as rethopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                                                                                                                                                                                                                                 Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antitheumatic; antiarthritic; antidiabetic; antipsoriatic; antilnflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1026; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                       Human immune system associated gene SEQ ID NO: 1026.
                                                                                                                                                  75187 GTAGTATAATAGTTATAAAAGAGAAATTTAAAG 75219
                                                                                                                      309 TGTGTTTTCTGACTATTGAGGGGCCAAAAAAAG 341
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ATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTAACAGAAACTTCCAAATTTTTT

0; Mismatches 141; Indels

Conservative

Local Similarity es 138; Conserv

Best Loca Matches

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87

Gaps

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267
                                                                                                                                                                                                                                                                                                                                          DNA transcription associated gene; peptide nucleic acid; PNA-oligomer; prA; cytosine methylation state; SNP; retroviral infection; gene; ds; single nucleotide polymorphism; adenosine deaminase deficiency; cancer; viral infection; Sezary syndrome; haematological disorder; tuberculosis; munuological disorder; Werner syndrome; developmental disorder; postiasis; Rieger's syndrome; neurological disorder; erythropotesis; neurological disorder; erythropotesis; myelodysplastic syndrome; myeoradial infarction; Nypertension; arthritis; anglogenesis; congenital heart disease; HDR syndrome; gene therapy; polyglutamine disorder; solid tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer, in particular an oligonucleotide or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical to the chemically pretreated DNA of genes associated with DNA transcription. The set of oligomer probes are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for
208 TAGTAGGTGTAATTAATAGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid tumours or cancer
                                                                                                       ATACATACATATACACGTACATAAATATATATCTTTTA 6589
                                                                          ATTAAAATATTAACTTTAAAATAAATAAAAATTTGAGTA 306
                                                                                                                                                                                                                                                                                                           DNA transcription associated genomic DNA #66.
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30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                     23-APR-2002 (first entry)
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                                                                        268
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(GENO-) GENOME THERAPEUTICS CORP

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                                                                                                                                                                                                                                                                                                                                                                                                      ATGACTTTTTTTTTTTCTACCACGGTGGATGAAAGTTATAGTACTATTAGCCAGAGACAAT 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAAAATTAGAAAATATAAAATATGAAAAATAGAGGAAAAGAGGTTTTAATTTATATATA 550
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                                                                                                                               infarction, hypertension, angiogenesis, erythropolesis, congenital heart disease, thR syndrome, arthritis, polyglutamine disorders, solid tumours or cancer. Sequences ABK28127-ABK28472 represent DNA transcription associated genomic DNA molecules of the invention.

Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGATTATAGATATCCATTAATCCATGATATTTATGATATAAATAGCTGTTAAACTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371 IGTTTATTAATGTATAGTTATTAAGGTATAAAGTTTGGGTTTATAGTTAGATAGTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTAAAAGGAGCATAACGAGGCAACAAAAGTAATGAACACGGAGAAACAAAAGCCATGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAGCATCGCAGCTTTCTGCAACTTTTGTTTTTAATTAAGAGTTTAATAAAAGTA
                                                                                                                                                                                                                                                                                                                                                                    Gaps
diagnosing or treating diseases associated with DNA transcription (particularly with the methylation status). e.g. adenosine deaminase deficiency, viral infection, retroviral infection, Sezary syndrome, haematological disorders, immunological disorders, Werner syndrome, tuberculosis, developmental disorders, psoriasis, Rieger's syndrome, neurological disorders, maurodegenerative disorders, Waardenburg syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial
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0
                                                                                                                                                                                                                                                                                                                              DB 24; Length 8170;
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                                                                                                                                                                                                                                                                                         Sequence 8170 BP; 2772 A; 69 C; 1274 G; 4055 T; 0 other;
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                                                                                                                                                                                                                                                                                                                          4.8%; Score 53.2; DB 24;
47.8%; Pred. No. 0.21;
Live 0; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATTATATTTCTGACTTCTTT 986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-2000; 2000US-0578900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 47.8 Matches 154; Conservative
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                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
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The invention relates to a method for identifying a molecule involved in lipid regulation comprising identifying a molecule that binds to or inhibits binding of a molecule to high bone mass (HBM) or its wild type gene, Zmaxi. Compounds identified by the method are useful for treating, ilpid-associated conditions, including arteriosclerosis, cardiovascular disease, stroke, and osteoprosis. The compounds may also be used in the treatment or prevention of diabetic atherosclerosis, neurovascular conditions caused by plaque build-up, poor circulation due to plaque build-up and associated poor wound healing. The methods may be used in gene therapy, pharmaceutical development, and diagnostic assays for bone development disorders. Molecules identified by comparison of Zmaxi and HBM systems can be used as surrogate markers in pharmaceutical development, in diagnosis of human or animal bone disease, and in the creatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA molecules encoding human Zmaxi and HBM, and PCR primers, probes, linkers and adapters of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 ACAGAAACTICCAAAITITITITITITITATGGA-ACAAGAAATAACAGAIAGAAAACTAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 TTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCT
                                                                                                                                    diagnosing, treating or preventing e.g., arteriosclerosis, comprises identifying a molecule that binds to high bone mass gene or its corresponding wild type gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 54108 BP; 11394 A; 14471 C; 15121 G; 13120 T; 2 other;
                                                                                                                     Identifying molecules involved in lipid requlation, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 24; Length 54108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human high bone mass (HBM) polynucleotide clone #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.2%; Pred. No. v...,
tive 0; Mismatches 155;
                                                 Recker RR, Johnson ML;
                                                                                                                                                                                                            Example 2; Page 284-323; 409pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.8%; Score 53;
                UNIV CREIGHTON SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK22784 standard; cDNA; 57273 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 TAAATGTGTTTTC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 50.2
Matches 157; Conservative
                                                 Little RD,
                                                                                  WPI; 2002-097784/13
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                                                 Carulli JP,
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                  (UYCR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
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lipid regulation comprision a method tor identifying a molecule involved in inhibits binding of a molecule to high bone mass (HBM) or its wild type gene, Zmaxi Compounds identified by the method are useful for treating, gene, Zmaxi. Compounds identified by the method are useful for treating, including arteriosclerosis, cardiovascular disease, stroke, and osteoporosis. The compounds may also be used in the conditions caused by plaque build-up, poor circulation due to plaque conditions caused by plaque build-up, poor circulation due to plaque gene therapy, pharmaceutical development, and diagnostic assays for bone HBM systems can be used as surrogate markers in pharmaceutical development, in diagnosis of human or animal bone disease, and in the creatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA cand adapters of the invention.
Human; mouse; Zmaxl; HBM; high bone mass gene; lipid regulation; stroke; lipid-associated condition; arteriosclerosis; cardiovascular disease; ss; osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up; bone development disorder; antiarteriosclerotic; cardiovascular; probe; osteopathic; cerebroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to a method for identifying a molecule involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGAAACTTCCAAATTTTTTTTTTTTTGGA-ACAAGAAATAACAGATAGAAAACTATT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 TIGTTGTGGAATGGAAGTAGTAATACATTAAGCAAATTTTAAAAAATTATATAAGCCT 184
                                                                                                                                                                                                                                                                                                                                                         Identifying molecules involved in lipid regulation, useful for diagnosing, treating or preventing e.g., arteriosclerosis, comprises identifying a molecule that binds to high bone mass gene or its corresponding wild type gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53; DB 24; Length 57273;
Pred. No. 0.31;
0; Mismatches 155; Indels 1
                                                                                                                                                                                                                                                                                                       Recker RR, Johnson ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 350-392; 409pp; English.
                                                                                                                                                                                                                                                                  (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
                                                                                                                                                                                                                                                     (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                               2001WO-US16946.
                                                                                                                                                                                                                         26-MAY-2000; 2000US-0578900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.8%;
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Best Local Similarity 50.22
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                     Little RD,
                                                                                                                                                                                                                                                                                                                              WPI; 2002-097784/13.
                                                                                                                                  WO200192891-A2
                                                                                                                                                                                           25-MAY-2001;
                                                                                                       Homo sapiens
                                                                                                                                                                06-DEC-2001,
                                                                                                                                                                                                                                                                                                  Carulli JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
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16174 TAATATACATTTATAAATACACATTTATATTTTTATATAAAATATATATAAAAATCTCC 16233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAAGCCT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 ATACGCGCTCAAAGTATGTTATCTAGTAGTGTAATTAATAATGCATGGTGCGATTCAGA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes the human Zmax1 gene and the high bone mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM genes have osteopathic activities. The genes can be used in gene therapy, antisense therapy and in the production of vaccines. They can be used in the diagnosis and treatment of bone disorders including osteoporosis, Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia. ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                   Human; high bone mass; HBM gene; Zmaxl gene; chromosome 11; 11q13.3;
sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
antisense therapy; vaccine; bone disorder; Paget's disease;
sclerostosis; osteomalacia; fibrous dysplasia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 66933 BP; 14237 A; 17817 C; 18323 G; 16556 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53; DB 22; Length 66933;
Pred. No. 0.32;
0; Mismatches 155; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modulating bone mass for the treatment of e.g. osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _ = = _ _ _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnson ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  high bone mass (HBM) and Zmaxl genes and
                                                                                                                                                                                                                        Human HBM gene region b200e21-h_contig4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 51; Page 308-350; 443pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recker RR,
                                                                                                                                   ABA82625 standard; DNA; 66933 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENO-) GENOME THERAPEUTICS CORP.
                                                          16234 AAGTIGCTITITC 16246
                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUN-2000; 2000WO-US16951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-2000; 2000US-0543771.
05-APR-2000; 2000US-0544398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.8%;
                              305 TAAATGTGTTTTC 317
                                                                                                                                                                                          25-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 50.2
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carulli JP, Little RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-657171/75
                                                                                                                                                                                                                                                                                                                                                          WO200177327-A1.
                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                       18-OCT-2001
                                                                                                                                                                   ABA82625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                      RESULT 13
                                                                                                                   ABA82625
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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the control of the modified sequences of the control may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as oligonoclectides and/or PNA-oligomers for particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL7011-ABL70626 represent chemically pre-treated genemic DNA's of genes associated with cell signalling.

Secultication, but is based on sequence information supplied by the
   Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genomic
                                                                                                 245 ATTGGGACAACAATGAAAACGGAATTAAAATATTAACTTTAAAATAAAATAAAAATTTGAG
                                   Length 16228;
                                                                                                                                                                                                                                                                                                                                                                                                               Cell signalling; cytosine methylation; cell signalling disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16228 BP; 4652 A; 198 C; 3601 G; 7777 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 349; 24pp+sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                               Chemically treated cell signalling DNA sequence#175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with cell signalling e.g. cancer, comprises chemica sequences of genes associated with cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.8%; Score 52.6; DB 24;
48.2%; Pred. No. 0.31;
1ve 0; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berlin K;
                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; tumour; cytostatic; ds.
                                                                                                                                                                                                                                                                                   ABL70459 standard; DNA; 16228
                                                                                                                                                                                                  30862 AAGTTGCTTTTTC 30874
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Conservative
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2000DE-1043826
                                                                                                                                                                  305 TAAATGTGTTTTC 317
                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-154758/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200202807-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                  01-JUL-2002
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                                                                                                                                                                                                                                                                                                                   ABL70459;
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                                                                                                                                                                                                                                                    RESULT 15
ABL70459/
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271154 ACATACTTATAAGTATATATTTAAAATATGTAATGTATATTTTTTAATGTATGTATA 27213
                                                 66 ACAGAAACTTCCAAATTTTTTTTTTTTTGGA-ACAAGAAATAACAGATAGAAAACTATT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGITGIGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes the human Zmaxi gene and the high bone mass (HBM) gene, which are found on chromosome 11q13.3. The Zmaxi and HBM genes have osteopathic activities. The genes can be used in gene therapy, antisense therapy and in the production of vaccines. They can be used in the diagnosis and treatment of bone disorders including
                                osteoporosis, Paget's disease, scierostosis, osteomalacia and fibrous dysplasia. ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 ACAAATTATTAATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTA
                                                                                                                                                                                                                                                                                                                                           Human; high bone mass; HBM gene; Zmaxl gene; chromosome 11; 11q13.3; sequence tagged site; STS; osteoporosis; osteopathic; gene therapy; antisense therapy; vaccine; bone disorder; Paget's disease; sclerostosis; osteomalacia; fibrous dysplasia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 72049 BP; 15164 A; 19306 C; 20142 G; 17434 T; 3 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Zmax1 genes and proteins useful the treatment of e.g. osteoporosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 72049;
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Pred. No. 0.32;
0; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Johnson ML;
                                                                                                                                                                                                                                                                                                                Human HBM gene region b527d12-h_contig309G.
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                                                                                                                                                                                                              ABA82623 standard; DNA; 72049 BP.
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                                                                                               305 TAAATGTGTTTTC 317
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Best Local Similarity 50.2
Matches 157; Conservative
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modulating bone mass for
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arch co	7 TCCAAAAAATTITGTTAACAGAAACTICCAAATTITTITITITITGGAACAAGAAAT	7 PACAGATAGAAAACTATTTTGTTGTGGAAGTAGTAATATACATTAAGCAAATTTT		7 TGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGAATTAAAATTTAACTTTAA 	7 AATAAATAAAAATTIGAGTAAATGTGTTTTCTGACTATTGAGGGGCAAAAAAAAGACAAT	7 GCCAAAA 353 	eted: June 10, 2003, 22:22:43 54.042 secs
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Sequence 2, Appli Sequence 2, Appli Sequence 63, Appl Sequence 1, Appli

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GENERAL INFORMATION:
APPLICANT: Typfer, R., Bautor, J., Bothmann, H., Filsak, E.,
APPLICANT: Hyricke-Grandplerre, C., Klein, B., Martini, N.,
APPLICANT: M. Iler, A., Schulte, W., Voetz, M., Walek, J.,
APPLICANT: Schell, J.
TITLE OF INVENTION: Promoters
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Datentin Release #1.0, Version #1.25 (EPG CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/617,860B
FILING DATE: 01-MAR-1996
PRIOR APPLICATION NUMBER: PCT/EP94/02950
FILING DATE: 05-SEP-1994
APPLICATION NUMBER: DE P4329951.2
FILING DATE: 04-SEP-1993
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036
COMPUTER READABLE FORM:
MEDIUW TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: IBM Compatible
COMPUTER: DOS. --- *1 0. Version #1.25 (
                            US-09-439-313-102
US-09-352-616A-102
US-09-352-616A-102
US-08-998-416-186
US-08-998-416-186
US-08-998-416-595
US-08-998-415-1
US-08-459-415-1
US-08-459-415-1
US-08-459-415-1
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US-08-459-415-2
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                                                                                                                                                                                                                                                                                                                                        US-08-821-994-63
US-09-419-459-1
                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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Patent No. 6133506
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TYPE: Nucleic acid
STRANDEDNESS: Double stranded
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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LOCATION: 2611..2613
FEATURE:
                                                    ANTI-SENSE: NO
ORIGINAL SOURCE:
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14, Appl
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Sequence 3, Appl
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/ptoTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/ptoTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-98-416-1137
US-08-98-416-1137
US-08-983-795A-36
US-08-947-823-1
US-09-641-638-651
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US-08-487-8268-13
US-08-232-463-14
US-08-213-463-14
US-07-867-116-2
US-07-91-867-8268-13
US-07-867-116-2
US-07-91-867-8268-13
US-07-91-867-8268-13
US-07-867-8268-13
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US-07-991-867B-8
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US-08-605-106-4
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                                                                   OM nucleic - nucleic search, using sw model
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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APPLICANT: Etzler, Judith B.
APPLICANT: Murphy, Judith B.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A NO. 6465716 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-0798100S
CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT FILING DATE: 1998-08-04
PRIOR PPLICATION NUMBER: US 08/907,226
                                                                                                                                                                                                                                                                                                                                                                                      66 ACAGAAACTICCAAAITITITITITITATGGAACAAGAAATAACAGATAGAAAACTATIT
                                                                                                                                                                                                                                                                           186 TACGCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 AAATGTGTTTTCTGACTATTGAGGGGCAAAAAAAAGACAATGCCAAAAGTCTACGGGTTT
                                                                                    Gaps
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                                                  Length 3350;
                                             Score 49.2; DB 3; Length 3
Pred. No. 0.02;
0; Mismatches 198; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1954 AATTGTCAATAACAGAAATAAACTAACACC 1925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366 GACTGTCCAGTTCGGTAATAATCTAATAAC 395
; LOCATION: join(2611..2908, 3001..3341)
US-08-617-8608-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09129112
Patent No. 6465716
GENERAL INFORMATION:
                                               4.58;
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                                                                Best Local Similarity 48.7
Matches 190; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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US-09-129-112-3/c
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LENGTH: 6265
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US-09-129-112-3
                                                 Query Match
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APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                         2936 TATITIATAGIGITITACIATICAAATAAACATAATGCAGATATGAAGITIACIG-AACT 2878
                                                                                                                                                                                                                           2757 TCACAACAAGTITGAAATITAATITAAAACTATATTATAAAATATTACCAAATACAITITAT 2698
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                                                                                                                                                                                                                                                                                                                                             135 AIGGAAGTAATATACATTAA--GCAAATTTTAAAAATTATATAAGCCTATACGCC 192
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                                                                                                193 TCAAAGTATGTTATCTAGTAGGTGTAATTAATA--ATGCATGGTGCGATTCAGAATTGGG
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     Length 6265;
Score 49.2; DB 4;
Pred. No. 0.023;
0; Mismatches 148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Israelsen, Ned REGISTRATION UNBER: 29,655
REGISTRATION UNBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION: (619) 235-8850
TELEPAX: (619) 235-6176
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2637 TITIATATTATCAATTAAGCAGACAA 2612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 TGTTTTCTGACTATTGAGGGGCAAAA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JMBER: US/08/487,826B
10-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/08487826B Patent No. 5993827
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
  4.5%;
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                         Best Local Similarity 53.13
Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
FILING DATE: 10-SER
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92660
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US-08-487-826B-13
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46 TICCAAAAAAATITITGITAACAGAAACTICCAAAITTITITITITAIGGAACAAGAAA 105
                                                                                                                                                                                                                                 106 TAACAGATAGAAAACTATTTGTTGTGGAATGGAAGTAGTAATATATACATTAAGGAAATTT 165
                                                                                                                                                                                                                                                                                              226 AIGCAIGGIGGGAITCAGAAIIGGGACAACAAIGAAAAGGGAAIIAAAAITAACIIIA 285
                                                                                                                                                                                                                                                                                                                                                 4.2%; Score 46.4; DB 4; Length 636;
48.8%; Pred. No. 0.055;
tive 0; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08451405A
Patent No. 5736358
GENERAL INFORMATION:
APPLICANT: FASEL, NICOLAS JOSEPH
APPLICANT: REXMOND, CHRISTOPHE DOMINIQUE
TITLE OF INVENTION: DICTYOSTELID EXPRESSION VECTOR AND
TITLE OF INVENTION: METHOD FOR EXPRESSING A DESIRED PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: THE WEBB LAW FIRM
STREET: TOO KOPPERS BUILDING, 436 SEVENTH AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB 1; Length 731;
Pred. No. 0.07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDITION OF THE STREET TOUR NOT THE STREET PERNOYELVARIA COUNTRY: UNITED STATES OF AMERICA ZIP: 15219-1818

" "FLOPPY DISK" " "FLOPPY DISK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-1995
N: 435
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK
COMPUTER: Midwest Micro 486-50
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/965,273 FILING DATE: 15-JAN-1993 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 AAATAAATAAAAATTT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
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                             636 base pairs
                                                                                                                                                    Query Match
Best Local Similarity 48.88
Matches 125; Conservative
                          LENGTH: 636 base pair
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                              ; ORGANISM: PAG1692RP
US-08-998-416-1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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Best Local Similarity
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US-08-451-405A-2
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                                                                                                                                                      69 GAAACTTCCAAATTTTTTTTTTTTTTGGAACAAGAAATAACAGATAGAAAACTATTTGT 128
                                                                                                                                                                                                                                          129 TGTGGAATGGAAGTAGTAATACATTAAGCAAATTTTAAAAATTATATAAAGCCTATAC 188
                                                                                                                                                                                                                                                                                                   189 GCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTG 248
                                                                                                                             ;
0
                                                                                     Length 19124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Steller, Christine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Knechtle, Philipp
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
WIMMER OF SEQUENCES: 1152
                                                                           Score 46.6; DB 2; Length 1
Pred. No. 0.12;
0; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No. 6239264artis Corporation
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Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
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Research Triangle Park
No. 6239264th Carolina
Y: USA
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INFORMATION FOR SEQ ID NO: 1137:
SEQUENCE CHARACTERISTICS;
                                                                     Query Match
Best Local Similarity 47.4%;
Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Philippsen, Peter
: Pohlmann, Rainer
: Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38,241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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MOLECULE TYPE:
HYPOTHETICAL:
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CLASSIFICATION:
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                           ; ANTI-SENSE;
US-08-487-826B-13
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Length 665;

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Query Match
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                                                                                             134
                                                                                                             135 ATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTC 194
                                                                                                                                                                                       142 GGAGTTTTTATTTGTATTTAAAATTATTAAACATAGTGAACCTAAAAATAGATTTGTG 201
                                                                                                                                                                                                                       195 AAAGTATGTTATCTAGTAGTGTAATTAATAGCATGGTGCGATTCAGAATTGGGACAA 254
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                                                 75 TCCAAATTTTTTTTTTTTTGGAACAAGAAATAACAGATAGAAAACTATTTTGTTGTGGA
                               Gaps
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APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant DNA Molecules and Expression
TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
                                                                                                                                                                                                                                                                                                                                              315 TTCTGACTATTGAGGGGCAAAAAA 340
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27-JUN-1997
27-JUN-1997
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Patent No. 5985607
GENERAL INFORMATION:
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NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (416) 364-7311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 665 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RY: Canada
M5H 3Y2
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 ATGITTATAATTAAATTTTATAATTAAATGTTTATAATTACATATTTATAATTAAA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     886 AGAAACAAAAGCCATGAAGCTCATTGGTTAGTTTAAGCTTAATAAGAAGATTTTATTAAA 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            335 ATGITTATAATT----ACATATTTATAATTAAAATGITTATAATTACATATTTATAA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        946 TITIAATGACGATGATAACAATTATATTTCTGACTTCTTTAAAACCCCCTCTTACAAA 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    546 GATICGIACGAICTAICTAATGACTITITITITITICTACCACGGIGGAIGAAAGTIATAGT
                                                                                                                                                                                                                                                                                                                                                         766 AAATAGCTGTTAAACTATTTCAGCATCGCAGCTTTCTGCAACTTTTGTTTTAATTTAAG
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Procedures and Materials for Conferring TITLE OF INVENTION: Pest Resistance in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING STSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
Score 45.8; DB 2;
Pred. No. 0.076;
0; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   023070-070210US
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APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-001-1996
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APPLICANT: Williamson, Valerie M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08947823
Patent No. 6114605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94111-000.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kaloshian, Isgouhi
APPLICANT: Yaqhoobi, Jafar
APPLICANT: Bodeau, John
APPLICANT: Milligan, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774 REFERENCE/DOCKET NUMBER: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
  4.28;
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                       Best Local Similarity 47.7 Matches 200; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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US-08-947-823-1
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LOCATION: 1570
OTHER INFORMATION: 10-509-295 : deletion of C
LOCATION: 1827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: 10-508-245
NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION: 10-509-284
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NAME/KEY: allele
LOCATION: 2048
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NAME/KEY: allele
LOCATION: 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: 10-511-62
NAME/KEY: allele
LOCATION: 2323
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LOCATION: 12854..13023
OTHER INFORMATION: exon 10
                                  LOCATION: 3124..3297
OTHER INFORMATION: exon 1
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LOCATION: 16567..16667
OTHER INFORMATION: exon 12
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LOCATION: 6349..6509
OTHER INFORMATION: exon 6
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LOCATION: 13308..13429
OTHER INFORMATION: exon 11
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LOCATION: 16775..16945
OTHER INFORMATION: exon 13
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LOCATION: 17063..17554
OTHER INFORMATION: exon 14
NAME/KEY: misc_feature
LOCATION: 17555..20674
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OTHER INFORMATION: exon 5
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OTHER INFORMATION: exon 9
                                                                                            OTHER INFORMATION: exon NAME/KEY: exon LOCATION: 5552..5633
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OTHER INFORMATION: exon
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LOCATION: 8645..8854
OTHER INFORMATION: exon
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LOCATION: 1128
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LOCATION: 5758
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LOCATION: 7379
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LOCATION: 2341
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JOCATION: 2832
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LOCATION: 1225,
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APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Coloumakov, Liya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BREEKS INVOLVED IN ARACHIDONIC ACID METABOLISM
TITLE OF INVENTION: GENERS INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE OF INVENTION: GENERS INVOLVED IN ARACHIDONIC ACID METABOLISM
CURRENT APPLICATION NUMBER: US/09/641,638
PRIOR APPLICATION NUMBER: US/09/502,330
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-24
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-24
PRIOR FILING DATE: 1999-03-25
PRIOR FILING DATE: 1999-03-35
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                                                                                                                                                                                                                                                             Length 51952;
                                                                                                                                                                                                                                               4.2%; Score 45.8; DB 3; Length 5
47.6%; Pred. No. 0.23;
tive 0; Mismatches 182; Indels
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OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 651, Application US/09641638 Patent No. 6432648
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 51952 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 47.6%
Matches 170; Conservative
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ORGANISM: Homo sapiens
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INFORMATION: 10-513-250 : polymorphic base A or
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                                                                                                                                                                                                                                                               : deletion of C
                                                                                                   OTHER INFORMATION: 10-513-352
NAME/KEY: allele
LOCATION: 2947
                                                                                                                                                        INFORMATION: 10-513-365
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NAME/KEY: allele
LOCATION: 7668
                                                    INFORMATION: 10-513-262
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                                                                    NAME/KEY: allele
LOCATION: 2934
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ION: 6183
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LOCATION: 6467
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LOCATION: 8658
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LOCATION: 8777
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LOCATION: 8608
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: One Liberty Place 46th Floor
Philadelphia
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Pred. No. 0.27;
0; Mismatches 180; Indels (
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APPLICANT: Chang, Andy C M
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostellum
CURRESPONDENCE ADDRESS:
                                                  : polymorphic base C or T
                                                                                                                                                                                                      : polymorphic base A or G
                                                                                                                                                                                                                                                          : polymorphic base A or C
                                                                                                                                                        : polymorphic base C or T
: polymorphic base G or
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        NAME/KEY: allele
LOCATION: 8926
LOCATION: 8926
LOCATION: 8926
LOCATION: 12171
LOCATION: 12171
LOCATION: 12171
LOCATION: 12181
LOCATION: 12429
LOCATION: 12429
LOCATION: 12429
LOCATION: 12429
LOCATION: 12429
LOCATION: 13341
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NAME/KEY: allele
LOCATION: 13492
                                                                                                                                                                                                                                                       OTHER INFORMATION: 10-507-321
NAME/KEY: allele
LOCATION: 13524
OTHER INFORMATION: 10-349-224
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                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 45.94
Matches 153; Conservative
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3925 ATTABACAATTTTTATAAATAAATATAAAACAACAACAAATAAAATAAAATACATTATCAT 3866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8865 GIGTAAATTACTITITGAAATTICTTATITITTATATACATATAACAATAAAAATGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
4.1%; Score 44.6; DB 2; Length 1
Best Local Similarity 47.3%; Pred. No. 0.33;
Matches 169; Conservative 0; Mismatches 184; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESSS:
ADDRESSEE: FOLLOW & Lardner
ADDRESSEE: ADDR
                                                                                                                                                 REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 235-6176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                               CLASSIFICATION: 435
ATTORNEY/AGENET INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ANTI-SENSE: NO
US-08-487-826B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-232-463-14/c
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APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 AATTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAACTATTTGTTGTGGAATGG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
4.1%; Score 44.8; DB 1; Length 3138;
Best Local Similarity 55.9%; Pred. No. 0.19;
Matches 85; Conservative 0; Mismatches 67; Indels 0
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AD90/00530
FILING DATE: 02-NOV-1989
ATTORIEX/AGENT INFORMATION:
NAME: PCCCATANATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1927 TritititaArrigGGTTTAAATTTCA 1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 TATGTTATCTAGTAGGTGTAATTAATAATGCA 230
                                                                                                                                                                                                                                                                                                                         NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET UNBER: RICE-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/487,826B FILING DATE: 10-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/08487826B
Patent No. 5993827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3138 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: NUCLEIC ACID
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     circular
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; NAME/KEY: CDS
; LOCATION: (3380)..(3720)
; NAME/KEY: CDS
; LOCATION: (3850)..(5835)
US-08-213-419B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock V
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                                                                                                                      Best Local Similarity
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TITLE OF INVENTION: GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: JII-002ACNCP
CURRENT APPLICATION NUMBER: US/08/213,419B
CURRENT FILING DATE: 1994-03-14
PRIOR FILING DATE: 1992-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 CAAGAAATAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 CAAATTTTAAAAAATTATATAAGCCTATACGCGCTCAAAGTATGTTATCTAGTAGGTGTA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 ATTAATAATGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGAATTAAAATATT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACTTTAAAATAAATAAAATTTGAGTAAATGTGTTTTCTGACTATTGAGGGGCAAAAAA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
4.0%; Score 44; DB:
Best Local Similarity 7.8%; Pred. No. 0.35;
Matches 20; Conservative 138; Mismatches
                                                                                                                                                    30472/114 IMMU
                                                  FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29.768
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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Patent No. 6333406
GENERAL INFORMATION:
APPLICANT: Inselburg, J. et al.
                                                                                                                                                                                                                TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                 REFERENCE/DOCKET NUMBER: 30.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1226 RRRRRRRRRRRRR 1211
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NAME/KEY: CDS
LOCATION: (2598)..(3404)
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                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
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720 ACAATTGATTATAGATATATCCATTAATCCATGATATTTATGATATAAATAGCTGTTAAA 779
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                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                             ó
Length 6124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith I
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
                                             0; Mismatches 132;
Score 43.8; DB 4;
Pred. No. 0.37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TORNEY/AGENT AND COME LONGO
NAME: Feeney, Joanne Longo
REGISTRATION UNBER: 35,134
RICE-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02 NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/07867106
Patent No. 5389526
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: RI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
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REGISTRATION NUMBER:
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                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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STATE:
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                                                                                                                                                                                  Gaps
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APPLICANT: Hall, Richard L.
APPLICANT: Hall, Michael B.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
CORRESPONDENCE ADDRESS:
                                                                                                                                                                               ö
                                                                                                                                                       Length 5852;
                                                                                                                                                    Score 43.6; DB 1; Length 5 Pred. No. 0.41; 0; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/991,867B FILING DATE: 12-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/657,584 FILING DATE: 19-FEB-1991 ATTONNEY AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 32, Application US/07991867B Patent No. 5476781 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,6
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              DNA (genomic)
                                                                                                                                                    Query Match
4.0%;
Best Local Similarity 48.4%;
Matches 121; Conservative
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PRIOR APPLICATION DATA:
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                                                     CDS
2378..5038
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                                                                                                           2378..5038
                                                                                                                                                                                                                                                                                                                                                                                                                                  968 TATATTTCT 977
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linear
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          MOLECULE TYPE:
ANTI-SENSE: NO
FEATURE:
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US-07-991-867B-32
TOPOLOGY:
                                                                  LOCATION:
FEATURE:
                                                     NAME/KEY:
                                                                                              NAME/KEY:
                                                                                                          ; LOCATION:
US-07-867-106-2
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992 CCCCTCTTACAAACAGAAGCTCCCTTTTTCAGTAGAAGTCCGATTCCCAATCTTAAAGAC 1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 TATAACAAAATAGCAATATAAGTAATATTATACTACCACATTCTATAGAATTTTTAAAT 327
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TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 40
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                                                                                                                                                                                                                                                                                                                                                                Length 660;
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                , DB 1;
0.29;
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2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                           Ouery Match 3.9%; Score 43.2;
Best Local Similarity 44.4%; Pred. No. 0.;
Matches 174; Conservative 0; Mismatches
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APPLICATION NUMBER: US/08/107,755A
FILING DATE: 19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 32, Application US/08107755A Patent No. 5721352
31,794
                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
                                                                                                                       INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 base pairs
                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: DNA (genomic) US-07-991-867B-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hall, Richard L.
                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                        nucleic acid
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COMPUTER READABLE FORM:
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APPLICANT: MOYER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
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992 CCCCTCTTACAAACAGAAGCTCCCTTTTTCAGTAGAAGTCCGATTCCCAATCTTAAAGAC 1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 660;
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PRICE TITON NUMBER: US 07/827,658
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTONNEY/AGENT INFORMATION:
NAME: Salivanchik, David R.
REGISTRATION NUMBER: 31,794
REFERNEK-DOCKET NUMBER: UF114.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 base pairs
TYPE: NUCLE of duble
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-107-755A-32
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Search completed: June 11, 2003, 01:53:47 Job time : 54.4398 secs Sequence 18370, Apple Sequence 18370, Apple Sequence 1931, Apple Sequence 196, Apple Sequence 5, Apple Sequence 5, Apple Sequence 51, Apple Sequence 111, Apple Sequence 111, Apple Sequence 10, Apple Sequence 199, Apple Sequence 199, Apple Sequence 190, Apple Sequence 190, Apple Sequence 190, Apple Sequence 110, Apple Sequence 10, Apple Sequence 110, Apple Sequence

Sequence 107, App Sequence 1036, Ap Sequence 252, App

US-10-072-349-252

ALIGNMENTS

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1109
7153
640681
6204
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7823
12405
15732
32463
428
8996
         11036
17848
364
960
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7195
7657
6306
7903
4985
6397
344
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45.8
45.8
45.6
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                                                                                             June 11, 2003, 01:50:19; Search time 158.028 Seconds (without alignments) 9750.738 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'cgn2_6'ptodata/1/pubpna/USO7_PUBCOMB.seq:*
'cgn2_6'ptodata/1/pubpna/USO6_WEW_PUB.seq:*
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'cgn2_6'ptodata/1/pubpna/USO9_WEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                       US-09-502-426B-1_COPY_2102_3202
                                                                                                                                                                                                                                                                                                 870385 seqs, 699768693 residues
                                                                - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_NA:*
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Match Length DB
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Maximum DB seq
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Perfect
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APPLICANT: Warren, Wesley C.
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathiagan, Nagappan
TITLE OF INVENTION: WUCLEIC ACLD AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: U5/20/960,352
CURRENT FILE OF SEQ ID NOS: 15112
SEQ ID NO 5785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 AACAGAAACTICCAAATTITITITITITAGGAACAAGAAATAACAGATAGAAAATT 124
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                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 156; Indels
                                                                                                                                                                                                                                                                                                       4.9%; Score 54.4; DB 10; 48.7%; Pred. No. 0.14;
Sequence 5785, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               al Similarity 48.7
                                                                                                                                                                                                                                                                                       NAME/KEY: unsure
LOCATION: (76),(9
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Best Local S
Matches 148
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Sequence 5785, Ap Sequence 558, Ap Sequence 7419, Ap Sequence 73, Appl Sequence 14, Appl Sequence 14, Appl Sequence 16, Appl Sequence 100, Appl Sequence 100, Appl Sequence 100, Appl Sequence 17, Appl Sequence 1183, Ap Sequence 1483, Ap Sequence 1483, Ap Sequence 6381, Appl Sequence 6381, Appl Sequence 6381, Appl Sequence 6381, Ap Sequence 11483, Ap Sequence 11484, Ap Sequence 11483, Ap Sequence 11484, Ap Sequence 11484, Ap Sequence 11419, Ap Sequ

US-09-129-112-3 US-10-239-676-100 US-10-224-562-3

5690 10286 12405 5689 6265 17419 53332

54.4 52.2 52.2 52.2 51.2 51.2 51.2 50.4 49.2 48.6 48.6

0 US-09-960-352-5785 1 US-09-960-352-558 0 US-09-960-352-7419 0 US-09-960-352-7419 0 US-09-960-352-1400 US-10-239-676-14 US-10-239-676-14 US-10-239-676-35 0 US-09-801-861-3 0 US-09-960-352-10265 US-10-199-846-1483 US-10-239-676-51 0 US-09-960-352-4637 US-10-199-846-6381 US-10-239-676-46

```
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OFHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 3400
                    APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUCLEIC AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                                                                                                                                                                            570 TATTAGCACGAATGGGTTTATTAATTTAAAAACTCACAACTTGATCAGATAAAATTTCAT 629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                            690 GGATGAAAGTTATAGTACTATTAGCCAGAGACAATTGATTATAGATATATCCATTAAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     750 ATGATATTATGATATAAATAGCTGTTAAACTATTTCAGCATCGCAGCTTTCTGCAACTT
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                                                                                                                                                                                                                                                                                                                                                 Length 377;
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                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Bos taurus
CTHER INFORMATION: Clone ID: 32-LIB3057-025-01-K1-H11
US-09-960-352-7419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 15-LIB3058-052-Q1-K1-D11
US-09-960-352-3400
                                                                                                                                                                                                                                                                                                                                             4.7%; Score 52.2; DB 10;
49.5%; Pred. No. 0.33;
ative 0; Mismatches 163;
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4.7%; Score 52.2; DB 10;
Best Local Similarity 46.7%; Pred. No. 0.35;
Matches 165; Conservative 0; Mismatches 188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3400, Application US/09960352 Patent No. US20020137139A1
    APPLICANT: Warren, Wesley C.
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APPLICANT: Warren, Wesley C.
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 49.5'
Matches 161; Conservative
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US-09-960-352-3400/c
                                                                                                                                                                                                    SEQ ID NO 7419
                                                                                                                                                                                                                            LENGTH: 377
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APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10299)C
CURRENT PILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NOS: 15112
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                                                                                                                   185 ATACGCGCTCAAAGTATGTTATCTAGTAGTGTAATTAATAATGCATGGTGCGATTCAGA
                                     16 ANTAITTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTAACAGAAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CRGANISM: Bos taurus
CTHER INFORMATION: CLone ID: 24-LIB3057-024-Q1-K1-F7
US-09-960-352-5558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 4.8%; Score 53.2; DB 10; Best Local Similarity 46.1%; Pred. No. 0.22; Matches 178; Conservative 0; Mismatches 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 TTCGGTAATAATCTAATAACTCTGTC 401
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                                                                                                                                                                                                                                                                                                     Sequence 5558, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
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Patent No. US20020137139A1
GENERAL INFORMATION:
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                                                                                                                                                                                                  160 TAAA 157
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Sequence 14, Application US/10239676
Fublication No. US2030082609A1
GENERAL INFORMATION:
APPLICANT: PIEPENBROCK, Christian
APPLICANT: DIER, Alexander
APPLICANT: DIERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019058.8
DE 10019058.8
DE 10032529.7
DE 10043826.1
FRIOR FILING DATE: 2001-04-06
2000-04-06
2000-04-06
2000-04-06
                                                                                                                                                                                                                                1542 TAAAACAATCTCAAAAAAAATATTAAACAAATTCTTAAAAATTAAATAAAACACCTCTCA 1483
  3630 TCCTTATTAATTTANATTAATTAACTTTATAAAACTACANAAATNANTAAAAA-TCAACT 3572
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                                        139 AAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTCAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: chemically treated genomic DNA (Homo saplens) US-10-239-676-14
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Pred. No. 2.1;
0; Mismatches 115; Indels
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Best Local Similarity 51.1%;
Matches 120; Conservative
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NUMBER OF SEQ ID NOS: 228
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LENGTH: 10286
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121 TATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAA 180
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APPLICANT: OLEK, Alexander
APPLICANT: DIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019058.8
DE 10013229.7
DE 100143826.1
PRIOR FILING DATE: 2001-04-06
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                                                        TGTTAACAGAAACTTCCAAATTTTTTTTTTTTTTGGAACAAGAAATAACAGATAGAAAAC
                                                                                                                                                                      19 ATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAAATTTTGTTAACAGAAACTTCCA
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FEATURE:
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LOCATION: (3186, 3188, 3522, 3568, 3584, 3586, 3591, 3616, 3840, 3846)
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US-10-239-676-73
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4.7%; Score 51.2; DB 9; Length 5690;
Best Local Similarity 49.3%; Pred. No. 1.5;
Matches 151; Conservative 0; Mismatches 154; Indels 1
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SEQ ID NO 73
LENGTH: 5690
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LOCATION: (381, 706,
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CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019173.8
DE 10019173.8
DE 10019473.8
DE 10019473.6
DE 10004386.1
PRIOR FILING DATE: 2001-04-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 4.6%; Score 50.4; DB 9; Length 5689; Best Local Similarity 52.2%; Pred. No. 2.2; Matches 157; Conservative 0; Mismatches 142; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: unsure
; LOCATION: (1818, 1930..1931, 1934..1935, 1947..1948, 1966)
US-10-239-676-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09129112
Patent No. US20020019995A1
                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 228
SEQ ID NO 90
LENGTH: 5689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1531 T 1531
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                                                                                                                                 APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BEBELIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT APPLICATION NUMBER: DCT/EP01/03968
DE 10019058.8
DE 10019058.8
DE 10032529.7
DE 10043826.1
PRIOR FILING DATE: 2001-04-06
2000-04-06
2000-04-06
2000-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8622 CCAAAAATTTTTTTTTTTTTAAAATAAAACTATTTCAACATATAAATA 8563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 TICCAAATTITITITITITATGGAACAAGAAATAACAGATAGAAAACTATTITGTTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 AATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATAAAGCCTATACGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 CAAAGTATGTTATCTAGTAGTGTAATTAATAATGCATGGTGCGATTCAGAATTGGGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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Pred. No. 2.
                                                                                  Sequence 35, Application US/10239676
Publication No. US20030082609A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 46.7%;
Matches 161; Conservative
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NUMBER OF SEQ ID NOS: 228
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LOCATION: (7895)
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GENERAL INFORMATION:
APPLICANT: Etzler, Marilynn E.
APPLICANT: Etzler, Marilynn E.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A No. US20020019995A1 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-079981UGS
CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT FILING DATE: 1998-08-04
PRIOR FILING DATE: 1997-08-06
PRIOR FILING DATE: 1997-08-06
PUWBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.1
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Sequence 90, Application US/10239676 Publication No. US20030082609A1 GENERAL INFORMATION:

RESULT

APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, Christian APPLICANT: BERLIN, Kurt

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Score 49.2; DB 9;
Pred. No. 5.8;
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                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                             4.5%;
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Best Local Similarity 49.0%;
Matches 129; Conservative (
                                                                                                                       Conservative
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US-10-224-562-3
                                                                                                        Best Local Similarity
Matches 173; Conserve
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| TC 10707
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     LENGIH: 17419
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LENGTH: 53332
                                                                                            Query Match
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Publication No. US20030082609A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEDENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
                                                                                                                                                                                                                                                                                                                                                 75 TCCAAATTTTTTTTTTTTTGGAACAAGAAATAACAGATAGAAAACTATTTGTTGTGGA
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                        OTHER INFORMATION: genomic sequence of NBP46 (DB46)
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CURRENT PILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 10043826.1
PRIOR FILING DATE: 2001-04-06
2000-04-06
2000-04-07
2000-06-30
2000-09-01
                                                                                                                                                                                                                                                   Score 49.2;
Pred. No. 3.
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ORGANISM: Dolichos biflorus
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(1617)..(1697)
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(1023)..(1151)
                                                                                                                intron
(1152)..(1559)
                                                                                                                                          exon
(1560)..(1616)
                                         exon
(633)..(944)
intron
(945)..(1022)
                                                                                                                                                                                         ) NAME/KEY: exon
; LOCATION: (1698)..(1790)
US-09-129-112-3
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SEQ ID NO 100
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Best Local Similarity
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                                      NAME/KEY:
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11007 TTACTITCTATITTATITACITATTCAAACTIACTICCTTITCCAALAACTITTAT 10948
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Sequence 3, Application US/10224562
Publication No. US200300222291
GENERAL INFORMATION:
APPLICAMT: VAN. Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THERE OF INVENTION: THERE OF UNDER: US/10/224,562
CURRENT APPLICATION NUMBER: US/10/224,562
CURRENT PILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
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FEATURE:

CHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-239-676-100
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                                                                                       Length 17419;
                                                                                                                     0; Mismatches 188; Indels
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: LOCATION: 365, 380, 389, 399, 404, 408, 413, 416, 429, 434, 435, 438,

: LOCATION: 440, 458, 473, 479, 490, 511, 519, 520, 522, 525

: OTHER INFORMATION: n = A,T,C or G

US-10-198-946-1483
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APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
PRIOR APPLICATION NUMBER: 06/3206,220
PRIOR FILING DATE: 2001-07-18
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                                                                                                                  Length 406;
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Pred. No. 2.5;
0; Mismatches 214; Indels
                                                                                                                                                        Indels
                  ; TYPE: DNA
... ORGANISM: Bos taurus
; OTHEN INFORMATION: Clone ID: 44-LIB3058-038-Q1-K1-C12
US-09-960-352-10265
                                                                                                            Score 48.4; DB 10;
Pred. No. 1.9;
0; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1483, Application US/10198846 Publication No. US20030099974A1 GENERAL INFORMATION:
                                                                                                                4.4%;
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Best Local Similarity 40.2%;
Matches 144; Conservative
                                                                                                                                    Best Local Similarity 50.09
Matches 121; Conservative
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US-10-198-846-1483
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SEQ ID NO 1483
LENGTH: 525
LENGTH: 406
                                                                                                                    Query Match
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Membling
APPLICANT: Tao, Membling
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(10298)C
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 10265
GENERAL INFORMATION:

APPLICANT: YAN, Chunhua et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL001098

CURRENT APPLICATION NUMBER: US/09/801,861

CURRENT FILING DATE: 2001-03-09

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGAATTAAAATTAAATTTAA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 AACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 TGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGAATTAAAATATTAACTTTAA 286
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Pred. No. 12;
0; Mismatches 134;
                                                                                                                                                        31431 AATATATAAATATATAAATATAT 31409
                                                                                                                                  AATAAATAAAATTTGAGTAAAT 309
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Patent No. US20020137139A1
                                                                                                                                                                                                                                                                     Sequence 3, Application US/09801861
Patent No. US20020119544A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 49.0%;
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-960-352-10265/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Human
US-09-801-861-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 3
LENGTH: 53332
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; ORGANISM: Artificial Sequence;
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-239-676-51
                                                                                                                                                                                                                                                                                                                                                2000-06-30
2000-09-01
NUMBER OF SEQ ID NOS: 228
SEQ ID NO 51
LENGTH: 9539
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US-10-239-676-51/c
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 51, Application US/10239676 Publication No. US20030082609A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 10032529.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10043826.1
                                             5903 ТААСТААТАААААААТТТААААААССААААТААААТТААААТААААЛААААСТТАААА 5844
                                                                                                  5963 AATTTTTCTAAAAAAAAAATTTAAAAATCAAAAATCTATTTAAACAAACAAAATA 5904
                                                                                                                                                        6023 АТТААААААТААТАГААААТСАААТТСТАААААТСАТААААААТСТААААААТТСААА 5964
207 CTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGG 266
                                                                                     147
                                                                                                                                          87
                                                                                                                                                                              27 AATAACAATGCATAGAAAGTTCCAAAAAAAATTTTGTTAACAGAAACTTCCCAAATTTTTT 86
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                                                                                                                                                                                                                                        Similarity
                                                                       ATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTCAAAGTATGTTAT 206
                                                                                                                            TTTTTTATGGAACAAGAATAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTTAAAAAATTATATAA 180
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                                                                                                                                                                                                                                   4.48;
                                                                                                                                                                                                                  0; Mismatches 150; Indels
                                                                                                                                                                                                                                   Score 48; I
Pred. No. 7
                                                                                                                                                                                                                                  DB 9; Length 9539;
7.9;
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Дb	Qy	Db
5783	267	5843
5783 ACAAACATAAAAATTCATACGACAAAACAAATTTAAAAAATTAACTT 5736	267 AATTAAAATATTAACTTTAAAATAAATAAAAATTTGAGTAAATGTGTT 314	5843 CTAAAAAATTCAAAAAAACAATAAAATATTTTAAAACTAAAATACGATTTAAAAAAA 5784
		4

Search completed: June 11, 2003, 08:07:37 Job time: 159.028 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  June 10, 2003, 22:03:39; Search time 2645.14 Seconds (without alignments)
10465.184 Million cell updates/sec
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1101
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

21	c 20	c 19	18	c 17	c 16	·c 15	c 14	c 13	12	11	10	9	c 8	c 7	6	5	c 4	c ω	2	_	Result No.
59	59.6	59.6	59.6	59.8	59.8	59.8	60.4	60.4	61	65	65	65	66.6	66.6	125	960.4	1090	1090	1101	1101	Score
5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.5	5.5	ნ. ნ	5.9	5.9	5.9	6.0	6.0	11.4	87.2	99.0	99.0	100.0	100.0	Query Match Length
664	547	547	422	358	358	358	507	507	553	528	528	450	469	469	826	1699	84196	84196	8889	6888	Length
29	64	33	3	58	27	25	64	$\frac{3}{3}$	22	27	25	17	64	ű	ר	18	<u>3</u>	27	19	1	DB
US-09-739-449-739	US-60-209-830-1402	US-09-873-402A-1402	US-09-865-419A-3041	US-60-145-485-6397	US-09-684-016-340019	US-09-654-617-340019	US-60-207-458-135967	US-09-865-439A-91952	US-09-565-306-29073	US-09-684-016-121875	US-09-654-617-121875	US-09-333-534-15000	US-60-207-458-84816	US-09-865-439A-40543	PCT-US99-22853B-3486	US-09-451-320-2050	US-09-803-736-1074	US-09-692-412-94	US-09-502-426-1	PCT-US00-03820-1	ID
Sequence 739, App	Sequence 1402, Ap	•	· Sequence 3041, Ap	Sequence 6397, Ap	Sequence 340019,	Sequence 340019,	Sequence 135967,	Sequence 91952, A	Sequence 29073, A	Sequence 121875,	Sequence 121875,	Sequence 15000, A	Sequence 84816, A	Sequence 40543, A	Sequence 3486, Ap	Sequence 2050, Ap	Sequence 1074, Ap	Sequence 94, Appl	Sequence 1, Appli	Sequence 1, Appli	Description

Oy 61 TGTTAACAGAAACTTCCAAATTTTTTTTATGGAACAAGAATAACAGATAGAAAAC 120	Query Match Query Match Best Local Similarity 100.0%; Pred. No. 2.4e-189; Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy AATCTACAAATTATTAATATTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAAA	22 59 59 5.4 2664 31 US-09-803-110-739 Sequence 739, App C 24 58.4 5.3 407 33 US-09-803-110-739 Sequence 739, App C 24 58.4 5.3 407 25 US-09-644-727-A-5263 Sequence 5263, App C 24 58.4 5.3 407 25 US-09-644-727-A-1141 Sequence 5263, App C 25 58.4 5.3 407 25 US-09-644-715-41141 Sequence 341141, C 25 58.4 5.3 407 25 US-09-644-715-41141 Sequence 341141, C 25 58.4 5.3 407 25 US-09-644-715-41141 Sequence 341141, C 25 58.4 5.3 407 25 US-09-644-715-41141 Sequence 341141, C 25 58.4 5.3 407 25 US-09-644-715-41141 Sequence 341141, C 25 58.4 5.3 407 25 US-09-644-715-41141 Sequence 341141, C 25 58.4 5.3 407 25 US-09-644-715-41141 Sequence 341141, C 25 58.4 5.3 407 25 US-09-644-715-41141 Sequence 341141, C 25 58.4 5.3 407 25 US-09-644-715-41141 Sequence 341141, C 25 US-09-644-715-41141 Sequence 341141, C 25 US-09-644-715-41141 Sequence 341141, C 25 US-09-644-715-41149 Sequence 341141, C 25 US-09-644-715-31406 Sequence 341141, C 25 US-09-644-715-31406 Sequence 341141, C 25 US-09-644-715-31406 Sequence 341141, C 25 US-09-644-717-31406 Sequence 341141, C 25 US-09-644-717-31406, C 29 US-09-644-717-6668 Sequence 341141, C 25 US-09-644-717-6668 Sequence 34114, App 144 US-09-711, C 25 US-0
RESULT 2 US-09-502-426-1 Sequence 1, Application US/09502426 GENERAL INFORMATION: APPLICANT: AZPIROZ, Ricardo APPLICANT: CHOE, Sunghwa FILLE OF INVENTION: DWF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF FILE REFERENCE: 2225-0001 CURRENT APPLICATION NUMBER: US/09/502,426 CURRENT FILING DATE: 2000-02-11 EARLIER APPLICATION NUMBER: 60/119,657 EARLIER FILING DATE: 1999-02-11 EARLIER FILING DATE: 1999-02-11 EARLIER FILING DATE: 1999-02-11	Qy 1021 CAGTAGAAGTCCGATTCCCAATCTTAAAGACAAAGCCATTAGAAAGAGAAAGTGAGTG	

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SOFTWARE: Patentin
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GAAGCTCATTGGTTAGTTTAAGCTTAATAAGAAGATTTTATTAAATTTTAATGACGATGA
                                                                              CAATTGATTATAGATATATCCATTAATCCATGATATTATGATATAAATAGCTGTTAAAC
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US-09-692-412-94/c
US-09-692-412-94/c
Sequence 94, Application US/09692412
GENERAL INFORMATION:
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Best Local Sin
Matches 1101;
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FILE REFERENCE: 38-10 (15493)C
CURRENT PAPLICATION NUMBER: US/09/692,412
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 124
SEQ ID NO 94
LENGTH: 84196
TYPE: DNA
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APPLICANT: Rounsley, Steven |
APPLICANT: Wiegand, Roger C.
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Similarity 99.9%;
O1; Conservative
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        ATCCTAAGGGTAATTTTGGAAATCCCAATTTAAACCGATTGAGACCGTACCGGACTTCCT
                                                               GGTTTGACTGTCCAGTTCGGTAATAATCTAATAACTCTGTCTTTGACCGCACGCTCGTGT
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Pred. No. 3.6e-187;
0; Mismatches 0;
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; OTHER INFORMATION: any n or Xaa = unknown US-09-451-320-2050
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US-09-451-320-2050
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Best Local Similarity
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS 42-59, 62-66, 68, FILE REFERENCE: 2750-0662P
CURRENT APPLICATION NUMBER: US/09/451,320
CURRENT FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 6998
SEQ ID NO 2050
LENGTH: 1699
LENGTH: 1699
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GENERAL INFORMATION:
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ORGANISM: Arabidopsis thaliana
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                                                                           CTNTTANCCANANACAATNGATTATAGATNTATCCATTAATCCATGATGATATTTATGATATA
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                                                                                         CTATTAGCCAGAGACAATTGATTATAGATATATCCATTAATCCATGATATTTATGATATA 766
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CHEN, Xianfeng
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Pred. No. 5.5e-164;
0; Mismatches 12;
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RESULT 7

US-09-865-439A-40543/c

Sequence 40543, Application US/09865439A

GENERAL INFORMATION:

APPLICANT: Edgertton, Michael D
APPLICANT: Hardeman, Kristine J.

APPLICANT: La Rosa, Thomas J.

TITLE OF INVENTION: Nucleic Acid Molecule
TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding FILE REFERENCE: 2750-0569F(PC)
CURRENT APPLICATION UNMER: PCT/US99/22853B
CURRENT FILING DATE: 1999-10-05
COTHARE: MS WOORD 97
COTHER INFORMATION: LOCATION 1..826, Ceres Seq. ID 1592085
COTHER INFORMATION: Any n = any nucleic acid, unknown or other
COTHER INFORMATION: any n = any nucleic acid, unknown or other
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GENERAL INFORMATION:
APPLICANT: Ceres,
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                               Molecules And Other Molecules Associated With
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/207,458
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 119126
SEQ ID NO 40543
LENGTH: 469
TYPE: DNA
                                                        SEQ ID NO 84816
                                                                                                                                                                                                                                                                                                                                   Sequence 84816,
                                                        CURRENT APPLICATION NUMBER: US/60/207,458
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 152/02
                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                                                                                       APPLICANT:
    ORGANISM: Zea mays OTHER INFORMATION:
                               TYPE: DNA
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                                           ENGTH:
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                                                                                                                                                     Xu, Nanfei
                                                                                                                                                                             Sammons, R. Douglas
Shukla, Hridayabhiranjan
                                                                                                                                                                                                                                                                                      Abad, Mark S.
Conner, Timothy W.
                                                                                                                                                                                                        Ruff, Thomas G.
                                                                                                                                                                                                                                   La Rosa, Thomas J.
Lalgudi, Raghunath V.
                                                                                                                                                                                                                       Ruan,
                                                                                                                                                                                                                                                            Hardeman,
                                                                                                                                                                                                                                                                          Deikman, Jill
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                                                                                                                                                                  Kunsheng
                                                                                                                                                                                                                       Yijun G
    Clone
                                                                                                                                                                                                                                                            Kristine J.
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  ID: LIB3355-005-P1-K1-G2
                                                                                                                                       NUCLEIC ACID MOLECULES
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                                                                                                                                      AND OTHER MOLECULES ASSOCIATED WITH
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US-09-654-617-121875
; Sequence 121875, Application US/09654617
; GENERAL INFORMATION:
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; Sequence 15000, Application US/09333534
; GENERAL INFORMATION:
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SEQ ID NO 15000
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 APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/333,534
CURRENT FILING DATE: 1999-06-08
NUMBER OF TO YOUR STANDARD OF TO YOU
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Conner, T
APPLICANT: Ruan, Yijun G.
                                                                                                                                                                                                                                                                                    ORGANISM: Arabidopsis thaliana
OTHER INFORMATION: Clone ID: LIB25-082-Q1-E1-E12
                                                                                                                                                                                                                                                                                                                TYPE: DNA
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Kovalic,
Jingdong
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50.1%;
                                                                                                                                                                                                                                5.9%; Score 65; 100.0%; Pred. No.
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              David K
                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acid Molecules and
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US-09-684-016-121875; Sequence 121875, Application US/09684016; GENERAL INFORMATION:
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; OTHER INFORMATION: unsure at all n locations
US-09-654-617-121875
                                                                                                      US-09-565-306-29073
; Sequence 29073, Application US/09565306
; GENERAL INFORMATION:
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; OTHER INFORMATION: unsure at all n locations
US-09-684-016-121875
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SEQ ID NO 121875
LENGTH: 528
TYPE: DNA
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SEQ ID NO 121875
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 38-21(15097)D CURRENT APPLICATION NUMBER: US/09/684,016 CURRENT FILING DATE: 2000-10-10 PRIOR APPLICATION NUMBER: US 09/654
                                       APPLICANT: Andersen, Scott | APPLICANT: Conner, Timothy W. APPLICANT: Lalgudi, Rashunath V. TITLE OF INVENTION: Nucleic TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Liu, Jin
TITLE OF INVENTION:
 TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15459)C
CURRENT APPLICATION NUMBER: US/09/565,306
CURRENT FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 528
TYPE: DNA
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                                                                                                Andersen, Scott E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kovalic, David K.
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                                                      Nucleic Acid
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%; Pred. No. 0.0
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 09/654,617
                                                         Molecules
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0.062;
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                                                        and Other Molecules Associated
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; OTHER INFORMATION:
US-09-565-306-29073
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                                                                                                                                                ; FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(507)
OTHER INFORMATION: unsure at
OTHER INFORMATION: Clone ID:
US-09-865-439A-91952
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                                                                                                            Query Match
Best Local
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LENGTH: 507
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                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: plants FILE REFERENCE: 38-21(51936)B CURRENT APPLICATION NUMBER: US/09/865,439A CURRENT FILING DATE: 2001-05-29 PRIOR APPLICATION NUMBER: US 60/207,458 PRIOR EILING DATE: 2000-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hardeman, Kristine J. APPLICANT: La Rosa, Thomas J.
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                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Zea mays
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106 TAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTT 165
                                           297
                                                                                              136;
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                                                                                                             Similarity
                                           TATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAA 180
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Pred. No. 0.42
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LIB3607-057-Q6-N6-H11
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Pred. No.
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Length

507; 0

Indels

Gaps

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RESULT 15
US-09-654-617-340019/c
; Sequence 340019, Application US/09654617
· GENERAL INFORMATION:
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; TYPE: DMA:
; ORGANISM: Zea mays
; OTHER INFORWATION: C
US-60-207-458-135967
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US-60-207-458-135967/c
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CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 152403
SEQ ID NO 135967
LENGTH: FCT
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Best Local :
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APPLICANT:
APPLICANT:
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Similarity 51.7%;
                                                                               AAAAAAAAAAAAAAAAAAAAA
                                                                                                 AAATAAATAAAATTTGAGTAAA 308
                                                                                                                     ATGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGAATTAAAATATTAACTTTA
                                                                                                                                                            AAATAAATAAAATTTGAGTAAA 308
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Sammons, R. Douglas
Shukla, Hridayabhiranjan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruan,
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La Rosa, Thomas J.
Lalgudi, Raghunath V.
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US-09-654-617-340019
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CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 463173
SEQ ID NO 340019
LENGTH: 358
TYPE: DNA
ORCANTO:
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Best Local S
Matches 151
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APPLICANT: Liu, Jine
TITLE OF INVENTION:
FILE REFERENCE:
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                     306 AAA 308
                                                                                                             186
                                                                126 TGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTA 185
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                                          TACGCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAA
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Pred. No. 0.51;
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Search completed: June 11, 2003, 05:00:37 Job time: 2648.14 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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  SUMMARIES
Sequence 1, Appli
Sequence 1, Appli
Sequence 35136, A
Sequence 35136, A
Sequence 4465, Ap
Sequence 46414, A
Sequence 776, Appl
Sequence 270, Appl
Sequence 2170, Appl
Sequence 2170, Appl
Sequence 1026, Ap
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Sequence 1103, Appl
Sequence 11, Appl
Sequence 9, Appli
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US-09-502-426B-1
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51.2	51.2	51.4	52	52	52	52	52	52	52	52.2	52.2	52.2	52.2	52.2	52.2	•	52.4	52.4	52.4	53	53	53
4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.8	4.8	4.8	4.8	4.8	4.8
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US-10-240-453-79	US-09-837-604A-245	US-10-205-189A-4914	US-09-947-916-240	US-60-466-412-84590	US-60-466-412-85572	US-60-466-412-84035	US-10-311-455-1709	US-10-257-166-121	US-09-615-606A-52378	US-10-087-192-1726	US-60-466-412-84704	US-60-465-241-51834	US-60-466-412-84370	US-60-465-241-51683	US-10-311-455-1829	US-10-257-166-129	US-10-311-506A-52	US-10-311-507-52	US-10-311-506-52	US-10-312-841-1	US-10-087-192-1408	US-09-949-016-14199
Sequence 79, Appl	Sequence 245, App	4914	Sequence 240, App			ro -	1709		Sequence 52378, A	$\mathbf{-}$			Sequence 84370, A	OD .		129,	52,	52,	ν.	e 1, A		Sequence 14199, A

ALIGNMENTS

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Y 241 CAGAATTGGGACAACAATGAAAACGGAATTAAAATATTAAACTTTAAAATAAAT	Y . 181 GCCTATACGCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAAT	Y 121 TATITTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAA 180 	y 61 TGTTAACAGAAACTTCCAAATTTTTTTTTTTTATGGAACAAGAATAACAGATAGAAAAC 120 	Y 1 AATCTACAAATTATTAATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAAA	Query Match 100.0%; Score 1101; DB 5; Length 6888; Best Local Similarity 100.0%; Pred. No: 8.9e-197; Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 1, Application US/09502426B GENERAL INFORMATION: APPLICANT: Azpiroz, Ricardo APPLICANT: Choe, Sunghwa APPLICANT: Feldmann, Kenneth A. TITLE OF INVENTION: DMF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF FILE REFERENCE: 11696-070001 CURRENT APPLICATION NUMBER: US/09/502,426B CURRENT APPLICATION NUMBER: US 60/119,657 PRIOR APPLICATION NUMBER: US 60/119,657 PRIOR APPLICATION NUMBER: US 60/119,658 PRIOR APPLICATION NUMBER: US 60/119,658 PRIOR FILING DATE: 1999-02-11 PRIOR PILING DATE: 1999-02-11 PRIOR FILING DATE: 1999-02-11 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 6888 TYPE: DNA ORGANISM: Arabidopsis thaliana	US-09-502-426B-1

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RESULT 2
US-09-502-426A-1
US-09-5024-426A-1
Sequence 1, Application US/09502426A
Sequence 1, Application US/09502426A
GENERAL INFORMATION:
APPLICANT: ACPIROZ, Ricardo
APPLICANT: CHOE, Sunghwa
APPLICANT: FELDMANN, Kenneth
TITLE OF INVENTION: DWF4 POLYNUCLEOTIDES, POLYPEPTIDES AND
FILE REFERENCE: 2225-0001
CURRENT APPLICATION NUMBER: US/09/502,426A
CURRENT FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/119,657
PRIOR APPLICATION NUMBER: 60/119,658
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Best Local S
Matches 1101
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 1
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ORGANISM: Arabidopsis
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Ol; Conservative
                                                                             GGTTTGACTGTCCAGTTCGGTAATAATCTAATAACTCTGTCTTTGACCGCACGCTCGTGT
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                                                    TCTAATGACTITTTTTTTTTCTACCACGGTGGATGAAAGTTATAGTACTATTAGCCAGAGA
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                                            TCTAATGACTTTTTTTTTTTCTACCACGGTGGATGAAAGTTATAGTACTATTAGCCAGAGA
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Pred. No. 8.9e-197;
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RESUIT 4
US-09-615-606A-35136/c
- Sequence 35136, Application US/09615606A
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; ORGANISM: Homo sapiens
US-60-466-412-85418
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; Sequence 85418, Application US/60466412
; GENERAL INFORMATION:
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: TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CLO01466
: CURRENT APPLICATION NUMBER: US/60/466,412
: CURRENT FILING DATE: 2003-04-30
: NUMBER OF SEQ ID NOS: 429241
SOFTWARE: FRASISEQ for Windows Version 4.0
SEQ ID NO 85418
LENGTH: 16885
TYPE: Nam
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Best Local Similarity
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                                                                                                               TTAAATTTTAATGACGATGATAACAATTATATTT 974
                                                                                                                                       CACGGAGAAACAAAAGCCATGAAGCTCATTGGTTAGTTTAAGCTTAATAAGAAGATTTTA 940
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48.2%;
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; Sequence 1465, Application US/09837604A
; GENERAL INFORMATION:
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TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15444)C
CURRENT FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 91663
SEQ ID NO 35136
              APPLICANT: De La Pena, Rôbert C. APPLICANT: Bougri, Olegs
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51892)B
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 CURRENT APPLICATION NUMBER: US/09/837,604A
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APPLICANT:
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NAME/KEY: unsure
LOCATION: (1)..(458)
OTHER INFORMATION: 1
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TYPE: DNA
ORGANISM: Glycine max
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Similarity 46.1%;
                                                               La Rosa, Thomas J.
Shukla, Hridayabhiranjan
De La Pena, Robert C.
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Nelson, Donald E.
Shukla, Hridayabhiranjan
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US-60-466-412-84116
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PRIOR APPLICATION NUMBER: US 60/197, PRIOR FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 81288
SEQ ID NO 1465
LENCTH: 592
TYPE: DNA
ORGANISM: Oryza sativa nipponbare
FEATURE:
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                                                                                                                                                                                      ; LENGTH: 23939
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-466-412-84116
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                                                                                                                                               Query Match 4.9%;
Best Local Similarity 50.0%;
                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 84116
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Best Local
                                                                                                                                                                                                                                                                 APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DET
FILE REFERENCE: CL001466
CURRENT FILING DATE: 2003-04-30
UNMBER OF SEQ ID NOS: 429241
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                                                  61 TGTTAACAGAAACTTCCAAATTTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAAC 120
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                       AAATTTTAAAAAATTTTTTTTTT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAATGCCAAAAGTCTACGGGTTT 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAAAAATTATATAAGCCTATACGCGCT----CAAAGTATGTTATCTAGTAGGTGTAATT 221
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                                                                                                                                               Score 54.4; DB 10; Pred. No. 0.45;
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NUMBER OF SEQ ID NOS: 2
SEQ ID NO 46414
LENGTH: 427
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 08/103,744
PRIOR FILING DATE: 1993-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 08/220,691 PRIOR FILING DATE: 1994-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 08/104,507
PRIOR FILING DATE: 1993-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/249,651 PRIOR FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/912,293
CURRENT FILING DATE: 2001-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Human Genes, Sequences, FILE REFERENCE: PO-100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1994-03-3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER:
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OTHER INFORMATION: n is
 NAME/KEY:
                                                                                                              NAME/KEY: misc_feature LOCATION: (36)..(36)
                                                                                                                                                           OTHER INFORMATION: n is
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                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                OTHER INFORMATION: n is
                                                            NAME/KEY: misc_feature
                                                                               FEATURE
                                                                                              OTHER INFORMATION: n is
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                                               OCATION:
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misc_feature
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                                                 (77)..(77)
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Best Local
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LOCATION: (424)...(424)
OTHER INFORMATION: n is equal to a,t,g,
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OTHER INFORMATION: n is
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JOCATION: (418)..(418)
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LOCATION: (364).:(364)
OTHER INFORMATION: n is
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LOCATION: (297). (297)
OTHER INFORMATION: n is
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OCATION: (372)..(372)
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OTHER INFORMATION: n is
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COCATION: (261)..(261)
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OTHER INFORMATION: n is equal to
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LOCATION: (212)..(213)
OTHER INFORMATION: n is
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LOCATION: (222)..(222)
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LOCATION: (191)..(191)
OTHER INFORMATION: n is
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LOCATION: (199)..(199)
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LOCATION: (139)..(139)
           208 TAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGA 267
                                                                           148
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                                                                                                                                                                                               al Similarity
137; Conserv
                                                           TATACATTAAGCAAATTTTAAAAAATTATATATAGGCCTATACGCGCTCAAAGTATGTTATC
                                    TTTTTATGGAACAAGAAATAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAA 147
                                                                                                                                (394).
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; Sequence 776, Application US/10311455
; GENERAL INFORMATION:
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ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 00/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-00
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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            APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System
FILE REFERENCE: 5013.1014
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CURRENT APPLICATION NUMBER: US/10/311,455
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SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 0.58;
1; Mismatches
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DB 7; 154;

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, NAME/KDY: misc_feature
; LOCATION: (1)...(148843
; OTHER INFORMATION: n =
US-60-466-412-86174
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PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 2424

SEQ ID NO 776

LENCTH: 6113

TYPE: DNA

PREAMISM: Artificial Sequence
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                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 86174, Application US/60466412
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 86174
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                                                                                                                                                                                                                                                                                                                                                      APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001466
                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                   TYPE: DNA
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Similarity 51.9%;
ACAAATTATTAATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTA 65
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Pred. No. 0.45;
1; Mismatches 154;
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Pred. No. 0.52;
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US-09-806-708B-22/c
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; NAME/KEY: promoter; LOCATION: (1)..(1141); OTHER INFORMATION: consensus sequence of A.t., US-09-806-708B-22
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CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: The University of British Columbia TITLE OF INVENTION: Regulation of Embryonic T: FILE REFERENCE: 4810-58741
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                                             TTTTGGAAATCCCAATTTAAACCGATTGAGACCGTACCGGACTTCCTGGGATTCTGCTGG
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                                                                                             AVTTTHTDWCYKTWMNTWYWDMMTTMBTTTTRNMTTSTNMTNNNNNMWACTNNNNNNWW
                                                                                                                                           ACATTTTCACTGTTCTACCCCTACTCGTGAGCCCACCCTTTTCCCATATCCTAAGGGTAA
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ilarity 11.38;
Conservative 343
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Pred. No. 0
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CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 2170
LENGTH: 37973
                                                                                                                                                     ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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US-10-311-455-2170/c
; Sequence 2170, Application US/10311455
; GENERAL INFORMATION:
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APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
FILE REFERENCE: 5013.1014
                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                674 TTTTTTCTACCACGGTGGATGAAAGTTATAGTACTATTAGCCAGAGACAATTGATTATAG 733
                                                                                                                       Similarity
                                 AAATTATTAATATTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WWRRABHRSWNMWWVKCRNKYMVSWHYHAMRYBKWABAVGCNNNWKDRMAHHHWCATNNN 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NWRBCKTTSWMWWMDHMNTHCTYGNNTWGSAYBMAAMSMWAAGASNBVTYNWCWRMTYMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTAGTTTAAGCTTAATAAGAAGATTTTAATTAAATTTTAATGACGATGATAACAATTATA 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MWKAACNNNNBKAMYMRVAWMYSRDTTNTDWMMWTSDWBWHWYTVDYTMMRAWNNNNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MRCRDVTYTRNNTYCKSYAHSYWYWSNNAMWYRRYSARNWSSMARWTTRNNWWMSGBYRM 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNNNNNNNNSCCTCTRMNTMRWTMKGDGMTVRKKVKWRDTTCTYVDVWADSWVWWYANW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCATTTATCAAAAATTATTAGCACGAATGGGTTTATTAATTTAAAAAACTCACAACTTGA
                                                                                                         Conservative
                                                                                                                    4.9%;
                                                                                                Score 53.8; DB 9;
Pred. No. 0.57;
0; Mismatches 157;
                                                                                                                         Length 37973;
                                                                                              Indels
                                                                                             1;
                                                                                         Gaps
                                                               67
                                                                                         1;
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CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-03
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1026
LENGTH: 17131
TYPE: DNA
                                                                                                                                                                                     δÃ
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                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: unsure
; LOCATION: 1691, 1725, 1811
; OTHER INFORMATION: n is a or g or c or
US-10-311-455-1026
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US-10-311-455-1026/c
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APPLICANT: DIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Det
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                       Local Similarity
                      6807
                                                                                                                                                                                                                   6867
268 АТТАЛАЛТАТТААСТТТАЛАЛТАЛАТАЛАЛАТТТGAGTA 306
                                                                                                                                                                  88 TITTTATGGAACAAGAAATAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAA 147
                                                                                                                                                                                                                           28 ATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTAACAGAAACTTCCAAATTTTTTT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8117 TITTTTTTTTTTTTTA 8101
                                                  TAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGA 267
                                                                                ACTAAAATAATCTAATTTTTAAAAAACCCTAAAATCATAAACATATTCTATATATTTTTCA
                                                                                                           TATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTCAAAGTATGTTATC
                                                                                                                                       TCTTAAACAATAATAAAAACATAAATATTCATCAAAATACTCTATAAACCTTTTCATTTA
                                                                                                                                                                                                89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACGCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAAT
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                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/10311455
                                                                                                                                                                                                                                                                                 4.98;
                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                            Score 53.4; DB 9; Pred. No. 0.7; 0; Mismatches 141;
                                                                                                                                                                                                                                                                                          Length 17131;
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RESULT 15
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; NAME/KEY: misc_feature
; LOCATION: (1)...(3297126)
; OTHER INFORMATION: n = A,T,C or G
US-09-947-916-332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-09-947-916-332/c
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Best Local
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              CURRENT APPLICATION NUMBER: US/10/240,453 CURRENT FILING DATE: 2002-10-02 PRIOR APPLICATION NUMBER: PCT/EP01/03973 PRIOR FILING DATE: 2001-04-06 PRIOR APPLICATION NUMBER: DE 10019058.8 PRIOR FILING DATE: 2000-04-06
                                                                                                                      TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA TITLE OF INVENTION: Transcription TITLE OF INVENTION: by Means of Assessing the Methylation Statile OF INVENTION: with DNA TRANSCRIPTION FILE REFERENCE: 5013.1009
                                                                                                                                                                                                                               APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/947,916
CURRENT FILING DATE: 2003-03-20
NUMBER OF SEQ ID NOS: 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED
TITLE OF INVENTION: 19, METHODS OF DETECTION, AND USES THEREOF
FILE REFERENCE: CL001296
                                                                                                                                                                                                                APPLICANT:
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TYPE: DNA
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APPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 GAATGGAAGTAGTAATATACATTAAGCAAATTTTTAAAAAATTATATAAGCCTATACGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 4.9%;
Similarity 48.5%;
47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTGGGAC
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                                                                                                                                                                                                                             PIEPENBROCK, Christian
NUMBER:
DE
10019173.8
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Pred. No. 0.55;
0; Mismatches 156;
                                                                                                                                                         Methylation Status of Genes Associated
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Search completed: June 11, Job time: 822.985 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 131
LENGTH: 8170
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Matches 154; Conser
                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR EILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 350
                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                            491
                                                                                                                                                      431
                                                                                                                                                                                   785
                                                                                                                                                                                                                 371
                                                                                                                                                                                                                                                                            311
                                                                                                                                                                                                                                                                                                         665 ATGACTTTTTTTTTTCTACCACGGTGGATGAAAGTTATAGTACTATTAGCCAGAGACAAT
                                                 GAAAAATTAGAAAATATAAATATGAAAAATAGAGGAAAAGAGGTTTTAATTTTATATATA
                                                                                                                                                                                                                 TGTTTATTAATGTATAGTTATTAAGGTATAAAGTTTGGGTTTATAGTTAGATAGTTTAAT
   AATTATATTTTCTGACTTCTTT 986
                                                                                                                          TTAAAAGGAGCATAACGAGGCAACAAAAGTAATGAACACGGAGAAAACAAAAGCCATGAAG
                                                                                                                                                      TGATTATAGATATCCATTAATCCATGATATTTATGATATAAATAGCTGTTAAACTATT
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                     4.8%;
                                                                                                                                                                                                                                                                                                                                                     Score 53.2; DB Pred. No. 0.79;
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB seq
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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10683.154 Million cell updates/sec
                Query
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em_gss_vrt:*
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em_estpl:*
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58.4	58.4	58.4	58.6	58.6	58.8	59	59	59.2	59.2	59.6	59.6	59.8	59.8	60	60	60.2	60.6	60.6	60.8	60.8	61	61	61.4	61.6	61.6	61.6	61.6	61.8	62	62.4	62.6	62.8	63.2	63.4	63.6	64.6	65.2	65.8	
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SN	CNS00CS1	CNS003XU	CNS00EO7	CNS0155H	CNS008X3	CNS04NOJ	CNS014PQ	CNS00CS1	CNS01U9O	BE420618	CNS020K7	CNS005ZC	CNS07E8R	CNS0161D	CNS04D0K	CNS016C2	CNS0039G	CNS0187R	CNS001FB	CNS00BO1	AG075009	CNS01G8P	CNS020K7	CNS016CO	CNS02ON7	CNS016LI	CNS025K2	CNS003BD	CNS01ZGM	CNS04P5D	CNS00EVL	CNS00587	CNS00BO1	CNS0021J	CNS021G2	CNS00EVL	100	CNS0021J	
AL071063 Drosophil	59666	5304	9440	5023	544	AL298972 Tetraodon				BE420618 HWM000.G0	AL175696 Tetraodon	AL061991 Drosophil	_	AL106171 Drosophil	w	v١	_	w	v	AL057419 Drosophil	AG075009 Pan trogl					AL106896 Drosophil	AL182171 Tetraodon	AL064091 Drosophil			Drosophi	153	9	936	843	706 Drosophi	78714	AL061936 Drosophil	

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ALIGNMENTS

SOURCE ORGANISM RESULT 1 BH811044/c LOCUS REFERENCE AUTHORS VERSION KEYWORDS COMMENT DEFINITION ACCESSION JOURNAL TITLE Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicottyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 148)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu BH811044 148 bp DNA linear GSS 02-MAY-20 SALK_057128 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_057128, DNA sequence. Arabidopsis Genome Unpublished (2001) thale cress. BH811044.1 S single pass sequence recovered from the left border of GI:20388862 GSS 02-MAY-2002 Shinn, P.

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145.6 69.6 69.4 66.8 66.4

13.4 13.2 6.3 6.3 6.1

148 473 1101 1201 1201 928 1201

17 17 17 17

BH811044
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CNS00DKY
CNS0165X

BH811044 SALK_0571 AL768954 Arabidops AL063921 Drosophil AL106396 Drosophil AL071865 Drosophil AL106335 Drosophil

Score

Match

Length

DB

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                                   Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone T3A5. The sequences are generated at the MPI for plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
                                                                                                                                                                                                          L1, r., Rosso, M., Strizhov, N. and Weisshaar, B.
Direct Submission
Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       transformed lines
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                                                                                                                                                                                                                                                                                bases 1 to 473)
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                                                                                                                                                                                                                                                                                                                     .M., Strizhov.N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
lanking sequence tag based reverse genetics
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
                    Location/Qualifiers
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/clone="SALK_057128"
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Pred. No. 6.6e-18;
D; Mismatches 0;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfiy.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda, Hexapoda, Insecta; Pterygota;
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="GK-082A08-011867"
/clone=1b="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
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/db_xref="taxon:3702"
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/strain="Columbia 0"
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Pred. No. 1.3e-17;
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   Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail: - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was collaboration with the European Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                               761
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                                                                                          Eukaryota; Metazoā; Arthropoda; Hexapoda; Insecta; Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                            Drosophila melanogaster genome survey sequence T7 end of BAC
BACN15M24 of DrosBAC library from Drosophila melanogaster (fruit
                                                                   Direct Submission
                                                                              Genoscope
                                                                                                                                  Drosophila melanogaster.
Drosophila melanogaster
                                                                                                                                                              AL106396.1 GI:5621701 GSS.
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                                                                                                                                                                                           genomic survey sequence.
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/clone_lib="RPCI-98"
/note="end: TET3"
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/db_xref="taxon:7227"
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Genome Project
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segref@genoscope.cns
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Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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AL071865
AL071865.1 GI:4948170
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                                                                                                                                                                                                                                                                                                                                                     TGACTTCTTTAAAACCCCCCTCTTACAAACAGAAGCTCCCTTTTTCAGTAGAAGTCCGATT
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Similarity 37.2%;
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/plasmid="pBeloBAC11"
/note="end : T7"
87 c 79 g
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/db_xref="taxon:7227"
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr -
Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster genome using these BACs. For further in Buffelon.
Please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Urosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                   821
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                             Drosophila melanogaster genome survey sequence SP6 end of BAC BACN15C02 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL106335
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                                                                                                  Drosophila melanogaster.
                                                                                                                                              AL106335.1 GI:5621422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T---TGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAG 181
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/db_xref="taxon:7227"
/db_ref="hack27A24"
/clone="back27A24"
/clone_lib="RPCI-98"
/note="end : T7"
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                                                                            Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                                 GSS.
                                                                                                                                                                                                                                                                      CNS0021J 1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR05N11 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton project grant.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                      fly), genomic survey sequence.
                                                          Genoscope
                                                                                                                                                                             Drosophila melanogaster.
                                                                                                                                                                                                                   AL061936.1 GI:4940214
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATAATGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGAATTAAAATATTAAC 281
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/note="end : SP6"
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/organism="Drosophila melanogaster"
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Pred. No. 0.0061;
9; Mismatches 13
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  National de Sequencage : segref@genoscope.cns.fr
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RESULT 8
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                                                                                                                                                                                                                     CNS00LT2 1101 bp DNA linear Drosophila melanogaster genome survey sequence TET3 BACR48P19 of RPCI-98 library from Drosophila melanog
                                       Genoscope.
       Submitted
                                                              Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                          Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAAATTATATAAGCCTATACG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAACTTCCAAATTTTTTTTTTTTTTGGAACAAGAAATAACAGATAGAAAACTATTTTGTT 129
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                                                                                                                                                                                                        genomic survey sequence.
                       Submission
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/clone="BACR05N11"
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7 c 28 g
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 (11-JUN-1999) Genoscope
                                                                                                                                       melanogaster.
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Pred. No. 0.0082;
                                                                                                                                                                                                                                                        1101 bp
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                                                                                                                              CNSQUEVL 1101 bp DNA linear GSS 04-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC: BACC-98 library from Drosophila melanogaster (fruit
               Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                     GSS.
                                                                                                     fly), genomic survey sequence AL069706
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                 Drosophila melanogaster.
                                                                                     AL069706.1
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GI:4949849

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      564 AAAAATTATTAGCACGAATGGGTTTATTAATTTAAAAACTCACAACTTGATCAGATAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
KGKKKAGDDDAKDKTKKKKKAATTTTKKKKGKKKKKAAKKKKAADRTKKTKWDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAATATTTTTTTKWTTWKATKTDWTKKAKTAAKTAAWAAWWTTTTTTAATWTTTTKTWT
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                                                   TTAATAAGAAGATTTTATTAAATTTTAATGACGATGATAACAATTATATTTTCTGA 979
                                                                                                                                                                                                                                                                                 CAACTTTTGTTTTTAATTTAAGAGTTTAATAAATAAAAGTATTAAAAAGGAGCATAACGAG
                                                                                                            KWDGAKKATKTKKKKDKKAAWAAADKKDRKKGGKKKGKKGKKGKKGKKGKKKKKKKKGKGGWGK
                                                                                                                                                                     GCAACAAAAGTAATGAACACGGAGAAAACAAAAGCCATGAAGCTCATTGGTTAGTTTAAGC
                                                                                                                                                                                                                              TAKTKTTTTTTTTTTATTAAATAAAAAAWTTTDTWAAAWWTTTKKKKKKAAAADKWKDAK
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/clone="BACR48P19"
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                                                               CNSUZIGZ I146 bp DNA linear GSS 12-MAY-Tetraodon nigroviridis genome survey sequence T7 end of clone 225004 of library G from Tetraodon nigroviridis, genomic survey
                                  sequence.
AL176843
                                                                                                              CNS021G2
            AL176843.1
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                                                                                                                                                                                                                                                                                                                                   AGAAACAAAAGCCATGAAGCTCATTGGTTAGTTTAAGCTTAATAAGAAGATTTTATTAAA 945
                                                                                                                                                                                                                                                                                                                                                                           AGTTTAATAAATAAAAGTATTAAAAAGGAGCATAACGAGGCAACAAAAGTAATGAACACGG
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/db_xref="taxon:7227"
/db_xref="BACR29B23"
/clone="BACR29B23"
/clone_lib="RPCI-98"
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91 c 60 g 299 t 232
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetracdon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetler,F., Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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Similarity 31.8%;
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                       ACGATGATAACAATTATTTTCTGACTTCTTTAAAACCCCCCTCTTACAAA 1004
                                                                                                                                                                                  AAATAAAAGTATTAAAAGGAGCATAACGAGGCAACAAAAGTAATGAACACGGAGAAACAA 893
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                                                                                                                                                                                                                                                                                                            KRRKKKRAAAAKKKBRKKTGRKGRRKGGRARKKGRGAARGAAGRRKKNKKGDAWATTTTD
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                                                             AAAANTTTKRRDKRTTTTTTDRTTTWWTTAAAAAAWTTWTTAWTTTTTATTATAAAWA
                                                                                                    AAGCCATGAAGCTCATTGGTTAGTTTAAGCTTAATAAGAAGATTTTATTAAATTTTAATG 953
                                                                                                                                              ACTTCCTGGGATTCTGCTGGAGCATTTATCAAAAATTATTAGCACGAATGGGTTTATTAA
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/db_xref="taxon:99883"
/clone="255004"
/clone_lib="G"
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60 c 73 g 274 t 346 others
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Score 63.6; DB 17; Pred. No. 0.021; 8; Mismatches 222;

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Determination with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                     122 ATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAA 180
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AL057419
AL057419.1
                                        Drosophila melanogaster genome survey sequence T7 end BACR24D09 of RPCI-98 library from Drosophila melanogas fly), genomic survey sequence
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-JUN-1999) Genoscope · Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope.
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/clone_lib="RPCI-98"
/note="end : TET3"
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/db_xref="taxon:7227"
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Pred. No. 0.023;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitffly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacnac.med.htm.ffalo.edu/Arococnilis has htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     558 TTTATCAAAAATTATTAGCACGAATGGGTTTATTAATTTAAAAAACTCACAACTTGATCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                        AATAAWTSTAMAATSVCASBSSVWTTATATTTTTASAAAWAWAKAWAATTTTSTGSTRT
                                                                                                                              TTTAAGCTTAATAAGAAGATTTTATTAAATTTTAATGACGATGATAACAATTATATTTTC
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/clone_lib="RPCI-98"
/note="end : T7"
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/db_xref="taxon:7227"
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51; Mismatches 1
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/db_xref-"taxon:7227"
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
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651 AAAAAAAAAAAAAAAWATWAATAATAATATTTAAAAATATTTATATATATAAAAAA	186 TACGCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGC		126 TGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAAATTATATAAGCCTA 185			:	TAATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAAA	y Match 5.7%; Score 62.4; DB 17; Length 855; Local Similarity 44.0%; Pred. No. 0.038; hes 153; Conservative 18; Mismatches 177; Indels 0; Gaps 0;	/Clone_1lb="G" /note="Genoscope sequence ID : COBG125DD10LP1~end : T7" 349 a 122 c 86 g 237 t 61 others	/org /db_ /clc	Location/Qualifiers 1855	nigroviri	tted (12-APR-2000) sequence is a single read and was gen	Genoscope. Direct Submission		Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis	Weissenbach, J.	E i.e	7 300000	Saurin, W. and Weissenbach, J. Human gene number estimate provided by genome wide analysis using	Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F.,	Tetraodontidae; Tetraodon. 1 (bases 1 to 855)	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;	Tetraodon nigroviridis Eukarvota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:	Tetraodon nigroviridis.) } }	, 90	Tetraodon nigroviridis genome survey sequence T7 end of clone 125H2O of libzary G from Tetraodon nigroviridis, genomic survey			368 CTGTCCAGTTCGGTAATAATCTAATAACTCTGTCTTTGA 406

Search completed: June 11, 2003, 06:58:35 Job time: 1673.1 secs

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SUMMARIES

Result No. Score 54.8 54.8 54.6 54.2 54.2 Match 100.0 99.6 33.8 33.8 116.2 116.2 115.8 115.8 115.5 115.5 115.5 115.5 115.5 115.5 115.5 3 93491 3 934980 3 123280 3 123280 3 123280 1 6657 1 67919 1 7138 1 187013 7 5678 7 107739 7 256172 7 310779 7 6657 5449 7560 73786 309233 5926 12356 169546 7351 24091 106993 349980 150903 133501 Length B AX344564 AC113218 AX251768 AX345224 AX251068 PFMAL139610 PFMAL1396 AX323841 ACC116920 AZC115582 AXZ51921 AX347392 AXZ51424 ACL16956 AX344567 AX346040 ACL16979 ACC005139 ACC005139 ACC014610 ACC1161690 ACC1161690 ACC1161690 ACC1161690 ACC1161690 ACC1161690 ACC1161690 AX281500 AC116967 AX344570 AC117076 AC116966 AX347029 AX346543 AX346125 AC107582 AC098557 AX346554 AX251264 AC004157 AX344930 ATT3A5 AF412114 Ħ AX345423 AX251501 AX347313 AX349113 AX251424 AC116956 AX344567 AX346040 AC116979 AC005140 AC114263 AC014263 AC01463 AC AC11426 AC12361 AL04918 AC098557 AF044216 Arabidops AL132979 Arabidops AF412114 Arabidops Description Dictyoste Dictyoste Sequence Sequence Sequence Sequence Sequence Dictyoste Dictyoste Sequence Dictyoste Mus muscu Plasmodiu Sequence Sequence Rattus no Rattus no Sequence Sequence Plasmodiu Sequence Sequence Dictyoste Plasmodiu Plasmodiu Plasmodiu Plasmotiu Dictyoste Drosophil Drosophil Sequence Rattus no Sequence Sequence Sequence Sequence Sequence Sequence Sequence Dictyoste

ALIGNMENTS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 4818) Choe, S., Dilkes, B.P., Fujioka, S., Takatsuto, S., Sakurai, A. and	ptophyta; Embry eudicotyledons; les; Brassicaces., Takatsuto,S	ntae; Stre liophyta; ; Brassica , Fujioka,	riridipla a; Magno cosids II to 4818) kes, B.P.	Eukaryota; Viridipla Spermatophyta; Magno Rosidae; eurosids II 1 (bases 1 to 4818) Choe, S., Dilkes, B.P.	REFERENCE
•		•	thaliana thaliana	Arabidopsis thaliana. Arabidopsis thaliana	KEYWORDS SOURCE ORGANISM
		41	GI:29353	complete cds. AF044216 AF044216.1 GI:2935341	ACCESSION VERSION
AF044216 4818 bp DNA linear PLN 25-JUN-2001 Arabidopsis thaliana steroid 22-alpha-hydroxylase (DWF4) gene,	p DNA li 2-alpha-hydroxy	4818 b steroid 2	thaliana	AF044216 Arabidopsis	AF044216 LOCUS DEFINITION

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                                                                                                                                                                                      4101 TTTTTTTGCCCAATGATATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (22-JAN-1998) Plant Sciences, University of Arizona, Tucson, AZ 85721, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choe, S., Dilkes, B.P., Azpiroz, R. and Feldmann, K.A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The DWF4 gene of Arabidopsis encodes a cytochrome P450 that mediates multiple 22alpha-hydroxylation steps in brassinosteroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant Cell 10 (2),
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                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                    GAGCTAGGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTAGTGTCGACACT
                                                                                                                     TTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGG
                                                                                                                                     TTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGG 180
                     ATTAAACCTTAAATGGGCTTTCTATAAGGCCCAATTATATTACGATTATAACAAAGTGAC
                                                      GAGCTAGGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACT
                                                                                                                                                                                                           TTTTTTTTGCCCAATGATATATAAAAATTTTGGATAAATATATTATTGGATATTCGTTTT 120
                                                                                                                                                                                                                                                                                         1566
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                                                                                                                                                                                                                                                                                                                                                                                                             D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *Translation="MFETEHHTLLPLLLLPSLLSLLLFLILLKRRNRKTRENLPPGKS
GWPFLGETIGTLKPYTATTLGDFMQQHVKYGKIYRSNLFGEPTIVSADAGLNRETLQ
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TLFVLDSWQQNSIFSAQDEAKKFTFNLMAKHINSMDPGEEETEQLKKEYVTFMKGVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                            {	t NYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPNGLPIR}
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EELREEHLETARAKKELGESELNWDDYKKMDFTQCVTNETLRLGNVVRFLHRKALKDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APLNLPGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:3702"
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/map="8 cM from nga6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="brassinosteroid biosynthetic enzyme"
/note="member of the cytochrome P450 superfamily;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="dwarf4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Ws-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Arabidopsis"
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i2. .2654,2746. .2824,2931. .3040,3795. .4398)
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AUTHORS
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                                   /gene="T3A5.10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.genoscope.cns.fr
on Jan 27, 2000 this sequence version replaced g1:6434247.
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mlps.blochem.mpg.de/proj/thal/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidoconic lobases 1 to 84196)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (25-JAN-2000) MIPS, at the Max-Planck-Institut fuer Blochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Marcel Salanoubat and Francis Quetier, Groupement d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue Gaston Cremieux, BP191, 91006 Evry Cedex, France;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana. Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bloecker, H., Mewes, H.W., Lemcke, K., Mayer, K.F.X., Quetier, F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana DNA chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACTTTTACTTCGTTTTTGATCCGAAGCAATAACAAATTGTCAAATACCAAACACAAG 4398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 84196)
                                                                                                                                                                                  KEAELEDFFQVAEKDLRNKLLECSMKYNFDFEKDEPLGGGRYEWVKLNP*
                                                                                                                                                                                                             QATNRGGIVARNSAGASETSVVIVRRRDSPPVEEQCQIEEEDSSVSCCSTSEEKSKRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis
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                                                                                                                                                                                                                                                                  translation="MAAVRRRERDVVEENGVTTTVKRRKMEEEVDLVESRIILSPCV/
                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="367bp LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="
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'number=3

'number=1

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RSLNPRIVTLGEYEVSLNRVEFANRVKNSLRFYSAVFESLEPNLDRSKEELRVERVL
FGRRIMDLVRSDDDNNKPGTRFGLMEEKEQWRYLMEKAGFEPVKPSNYAVSQAKLLLW
NYNYSTYLYGIVEFSOCFICT ARMINIOTITEGERE"
                                                                                                                                                                                 GWPFLGETIGYLKPYTÄTTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQ

MEGRLFECSYPRSIGGILGKWSMLVLVGDMHDDMRSISLNFLARRLFILLKDVERH

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APLNLPGTAYMKALQSRATILKFIERKMEERKLDIKEBDQEEEEVKTEDDEAEMSKSDH

VRKQRYDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Contains Cytochrome P450 cysteine heme-iron ligand signature AA455-464; Prokaryotic membrane lipoprotein lipio attachment site AA320-330"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="T3A5.40"

complement(join(26093. .26338,27091. .27200,27308. .27386,

27478. .27570,27723. .28037,28136. .28288,28374. .28698,
                                                                                                                        EELREEHLETARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRELHRKALKDVRYKGYDIPSGWKVLFVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(18303.
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/note="similarity to predicted proteins, Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (15902.
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                                                                                                                                                                                                                                                                                                                                        translation="MFETEHHTLLPLLLLPSLLSLLLFLILLKRRNRKTRFNLPPGKS/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
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/gene="T3A5.10"
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/gene="T3A5.10"
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Best Local
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                                                        357;
Similarity
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                  complement(40243. .40336)
                                                                                                                                                                                                                                                                                                                                                                                           complement(40180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="U1 snrnp 70K protein"
/product="U1 snrnp 70K protein"
/protein 1d="CAB62436.1"
/db_xref="G1:6561970"
/ta_sref="G1:6561970"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(38307...38796,38877...39090,39189...39:
40180...40742,40337...40401,40489...40564,40655...4073
40805...40919,41225...41323))
/note="Contains Eukaryotic putative RNA-binding region RNP-1 signature AA179-186"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (39189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(39091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDRYSHRYDKMEEDDFRYEREYKRSKRSESREYVR"
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VPNWRPRRLGGGLGTSRVGGGEE I VGEQQPQGRTSQSEEPSRPREEREKSREKGKERE
RSRELSHEQPRERSKDRPREDKHHRDRDQGGRDRDRDSRRDRDRTRDRGDRDRDRDRDRDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(28779.
                                                                                                                                                                                                                                                                                                         /number=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (39271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(38877.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38307. .41323
/gene="T3A5.50"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (28699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(28374.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(28136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(28038.
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                                                                                                                                                                                                             99.6%;
99.7%;
                                                                                                                                                                                    0;
                                                                                                                                                                                 Score 356.4; DB 8
Pred. No. 4.7e-51;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .39270)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .38796)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             .40179)
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                                                                                                                                                                                                                                                                                                                                                                                                 .40242)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .27386)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 28698)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 28135)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28037)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 27570)
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                                                                                                                                                                                                                                         Length 84196;
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SOURCE
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JOURNAL
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JOURNAL
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Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Cheuk, R., Chen, H., Kim, C.J., Mossema, E., Meyers, M.C., Banh, J., Bawser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Kariin-Neumann, G., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Kariin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Panyis, P. W., Sakurai, T., Sandari, T., Yu, G., Yu, S., Shinozaki, K., Panyis, P. W., Sandari, R., Yangamura, Y., Yu, G., Yu, S., Shinozaki, K., Panyis, P. W., Sandari, R., Yangamura, Y., Yu, G., Yu, S., Shinozaki, K., Panyis, P. W., Sandari, R., Yangamura, Y., Yu, G., Yu, S., Shinozaki, K., Panyis, P. W., Sandari, R., Yangamura, Y., Yu, G., Yu, S., Shinozaki, K., Panyis, P. W., Sandari, R., Yangamura, Y., Yu, G., Yu, S., Shinozaki, K., Panyis, P. W., Sandari, R., Yangamura, Y., Yu, G., Yu, S., Shinozaki, K., Panyis, P. W., Sandari, R., Yangamura, Y., Yu, G., Yu, S., Shinozaki, K., Panyis, P. W., Sandari, R., Yangani, 
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Cheuk, R.

(SSP/Salk) and

Seki, M. (RIKEN GSC)

contributed equally

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                                                                                                                                                                                                                                           Olek, A., Plepenbrock, C. and Berlin, K. Diagnosis of diseases associated with the immune system Patent: WO 0200928-A 1614 03-JAN-2002; Epigenomics AG (DE)
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//db_xref="GI:15724348"
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/note="chemically treated genomic DNA (Homo sapiens)"
1 90 c 1299 g 2914 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RAFL06-76-F19(R13551)"
/note="ecotype: Columbia"
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/db_xref="taxon:3702"
/chromosome="3"
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Score 58; DB 6
Pred. No. 0.68;
0; Mismatches
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TITLE
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                                AC107582
AC107582.3 GI:21736513
                                                                   AC107582 173786 bp DI
Rattus norvegicus clone CH230-29B17,
***, 92 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olek,A., Piepenbrock,C. and Berlin,K. Diagnosis of diseases associated with the immune system Patent: WO 0200928-A 1196 03-JAN-2002;
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                                                                                                                                                                                                                      GATAAATT 3035
                                                                                                                                                                                                                                                                                                                             ACTATTAAAACCTTAAATGGGCTTTCTATAAGGCCCAATTATATTACGATTATAACAAAGT 297
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/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
47 c 1554 g 3805 t
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carron, T.F., Bulker, Bulker, C., Burrell, K., L., Byrd, N.C., Chen, G., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Falls, T., Eerarguto, D., Edwards, C.C., Elhaj, C., Escotto, M., Farnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Garrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, K., Harris, K., Harris, K., Harris, C., Harris, K., Harris, K., Harris, C., Harris, C., Harris, K., Holloway, C., Hollins, B., Homsi, F., Howard, S., Hober, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Kralsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Li, J., Li, Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Netzer, M., Ned, D., Nettson, N., Nettson, N., Nguyen, N., Nettens, N., Pate, A., Bayton, B., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Surton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Surton, A., Warten, R., Wang, S., Warten, R., Wang, S., Wallalmans, G., Wallamas, A., Walczyk, A., Wang, S., Wallamas, G., Wallamas, A., Walczyk, A., Wang, S., Wallans, S., Wallalams, G., Wallams, A., Walczyk, R., Wooden, S., Warten, R., Waoden, S., Watlington, C., Wallangon, A., Walczyk, R., Wooden, S., Warten, R., Waoden, S., Watlington, S., Wallangon, A., Walczyk, R., Wooden, S., Watlington, S., Wallangon, S., Wallangon, A., Walczyk, R., Wooden, S., Wallangon, S., Walson, D., Watson, J., Pote, S., Walson, R., Wang, O., Wallangon, S., Walson, D., Walson, R., Wang, O., Wallangon, S., Walson, D., Walson, R., Wang,
                                                                                                                                                                                                                                     Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                   Submitted (23-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 173786)
                                                                                                                                                                                                                                                                                                                                        Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Worley, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burkett, C., Burrell, K.L., Byrd, N.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                           Jul 12, 2002 this sequence version replaced
                                                             (bases 1 to 173786)
        Sequencing vector: plasmid; Chemistry: Dye-terminator B
                                                                                                                                                                      Center: Baylor College of Medicine Center code: BCM
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                                                                                                                                                                                                                                                                                                                    Submission
                                                                                                                                                                                                                ----- Genome Center
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                                           Summary Statistics
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Big Dye: 100% of reads
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 92 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as soon as i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: Phrap; version 0.990329
Consensus quality: 85701 bases at least Q40
Consensus quality: 94901 bases at least Q30
Consensus quality: 103067 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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                                                                                                Center project Information Center project name: GHJV Center clone name: CH230-81P10
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     Sequencing
                                                                                                                                                                                                                                                     Contact: hgsc-help@bcm.tmc.edu
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
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NOTE: This is a 'working draft' sequence. It currently consists of 61 contigs. The true order of the pieces is not known and their order in this sequence record is
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Consensus quality: 233927 bases at least Q30
Consensus quality: 234451 bases at least Q20
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Sequence 232 from Patent W00168912.
AX251264
                                                                                                          Patent: WO 0168912-A 232 20-SEP-2001; Epigenomics AG (DE)
                                                                                                                                                                                  artificial sequences.
1 (bases 1 to 12356)
Olek,A., Piepenbrock,C. and Berlin,K.
                                                                                                                                                                                                                                           synthetic construct
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Diagnosis of diseases associated with the
Patent: wo 0200928-A 1625 03-JAN-2002;
Epigenomics AG (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthetic construct.
synthetic construct
artificial sequences.
                                                                                                                                                                 Diagnosis of diseases associated with tumor suppressor genes and
                                                                                                                                                                                                                                                            synthetic construct.
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milarity 48.2%;
Conservative
/organism="synthetic construct"
/db_xxef="taxon:32630"
/note="chemically treated genomic 68 c 2127 g 6516 t
                                                                        Location/Qualifiers
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/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
55 c 1318 g 2991 t
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Score Pred.

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* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
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Plasmodium falciparum chromosome 12
PROGRESS ***, 2 unordered mini-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-FEB-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hyman, R.W., Fung, E.L., Qin, F., Rowley, D., Kurdi, O.B., Conway, A.B. and Davis, R.W. Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum Plasmodium falciparum
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Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                                                       Similarity
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                                             as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                           /organism="Plasmodium falciparum'
/db_xref="taxon:5833"
/chromosome="12"
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15381 c 1
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                                                                                                                                                                                                                                                                                                 23466: contig of 23466 bp in length
23666: gap of unknown length
169546: contig of 145880 bp in length
                                                                                                                   15.5%;
51.6%;
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                                                                                                                     Score 55.6;
Pred. No. 0.
                                                                                                       Mismatches
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3D7, ***
                                                                                                                                  Length 169546;
                                                                                                       Indels
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SEQUENCING IN
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                                                        RESULT 12
AX281500
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SOURCE
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Matches 157
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synthetic construct
artificial sequences.
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Sequence 1 from Patent W00200928
AX344930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent: WO 0200928-A 1 03-JAN-2002; Epigenomics AG (DE)
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AX281500.1
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/db_xref="taxon:32630"
/note="chemically treated genomic
42 c 1230 g 3849 t
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1. .7351
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GI:16608755
                            from Patent W00177376
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Pred. No.
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170;

0

Gaps

linear

PAT 02-NOV-2001

4064 319 259 3944 3884

Length 7351;

DNA (Homo

sapiens)"

the

immune

system

linear

PAT 01-FEB-2002

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REFERENCE
AUTHORS
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AC116967/c
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JOURNAL
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TITLE
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Best Local
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                                                                                                                                                                                                                                           AUTHORS
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Biotechnology, Beutenberstr. 11, Jena 07745, Germany
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
CDS predictions from GeneID may contain errors. Further Information
is available from IMB Jena, Department of Genome Analysis
                                            Submitted (04-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
                                                                                Baumgart,C.
Direct Submission
                                                                                                                                                                                                    Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P.,
Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K
Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
                                                                                                                                                                                                                                                                                          Dictyostelium discoideum.
Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                          AC116967

93491 bp DNA linear HTV
Dictyostelium discoldeum chromosome 2 map 5401525-54951
AX44, *** SEQUENCING IN PROGRESS ***, in ordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olek,A., Plepenbrock,C. and Berlin,K. Diagnosis of diseases associated with metastasis Patent: WO 0177376-A 164 18-OCT-2001;
                                                                                                                                       The
                                                                                                                                                       Unpublished
                                                                                                                                                                      Sequence and Analysis of Chromosome 2 of Dictyostelium
                                                                                                                                                                                                                                                                      Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                              AC116967
AC116967.1
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synthetic construct
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                                                                                                                                  Dictyostelium Genome Sequencing
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/db_xref="taxon:32630"
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Pred. No.
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                                                                                                                                    Consortium
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5401525-5495014 strain
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                          Olek,A.,
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NOTE: This is a 'working draft' sequence.

This sequence will be replaced
by the finished sequence as soon as it is available
the accession number will be preserved.
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/note-"chemically treated genomic DNA (Homo sapiens)-Original length of seq 1: 3.673778 <223>-split as sapiens)-Original length of seq 1: 3.673778 <223>-split as follows.-seq 01 0.000.001 To 0.349.980-seq 02 0.300.001 649.980-seq 03 600.001 949.980-seq 04 900.001 1.249.980-seq 05 1.200.001 1.549.980-seq 06 1.500.001 1.849.980-seq 07 1.800.001 2.149.980-seq 08 2.100.001 2.449.980-seq 09 2.400.001 2.749.980-seq 10 2.700.001 3.049.980-seq 11 3.000.001 3.349.980-seq 12 3.300.001 3.649.980-seq 13 3.600.001 3.673.778 <223>-Original length of seq 2: 3.673778 <2223-split as follows.-seq 14 0.000.001 TO 0.349.980-seq 15 0.300.001 649.980-seq 16
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/db_xref="taxon:32630"
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/strain="AX4"
/db_xref="taxon:44689"
/chromosome="2"
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1 (bases 1 to 123280)

Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P.,
Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K
Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC117076 123280 bp Dictyostelium discoideum chromosome AX4, *** SEQUENCING IN PROGRESS ***,
                                                          Submitted (21-MAY-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis
                                                                                                                                                                                              Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 3 (bases 1 to 123280)
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HTG; HTGS_PHASE2.
                  (http://genome.imb-jena.de/dictyostelium/)
and the Univerity Colonge, Institute for Biochemistry I
                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                 Sequence and Analysis of Chromosome 2 of Dictyostelium
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(http://www.uni-koeln.de/dictyostelium/project.shtm/
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* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
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GPPKLVLPTNIRISQESQDLMNKMLSNELEESTDEEDISNLNKKSPFITGNNNNNNN
NNNNNNNNNNNNNNNNNNNNHKPLDLHQELGNIITEKFEXVTFEKLSLADRVCIANVDNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFNLDWMNLSNISVYKKPIFNNVIGNIGTTTTTTTTTTTTTTTTTTTTTNTINNTNVPEIPK
INLGTFKDSKRLHNHESAVTCIESDEAGFISGSQNGLVLRWDF*
complement(join(4915. .8220,8335. .8532,8632. .9345))
/note="ORF_ID:dd_03106"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEKKIKFWNLNTGQCIGDYEGESGYLSVEYDHTQKSSCIWPLSDYTKVHIGHKNGTVT
MVDFIEQPIEVIHTSRPTNLADGFDFTFPGKYLIWEHTIIHYWDVETSTLLWNELNAH
TKKITQSKIVAQHELSNKGIVFTTSSDKSAKVWDLTNGTCINTLVGHSYAVNCIEPIG
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sshergisvlskgvaeewispemmyellldisskskmpehcreahiieexdblunhiihl
nethplisulmulyrsckrupderleviamsielldegudofeclemgwulogted
okdkckmtfvogcdlrdieldripgyksfnskerledfoftflfpatvsgrlakifes
                       PSETFNNTVLSKENDFKPYVVEVWGIN"
                                                                                 SHNNIRSLVSSDSLASSFDETFSTTPKLLQDQTKYQFQEKILMTPEIYKKLRHYLPIR
                                                                                                                                 GINGSSYGGIGNDNNSKYKSKYKSKKEEEEHDAFIQKEISKLNLMEEEEEEMTYTDEIT
GANKKYLLFPCIYAIIHKDNSIQTLFFRGSDPTSVHTCFSYLKQLIYDSKFSPQTSSP
                                                                                                                                                                                                  GNSISNNPITNNKPPIHIPFSATSREERISKESIVKEKLVCFMRNQKVVGHLTLTPYQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRHITSLSWNTQETNLIASASSDCMANIFDIRERTQGSGGISTNFKARSNLSQIAWNP
NSSTMLATSNASEFNIWDIRKFGSPLSCVSAHIGSISNIEWSPKERNQLLTCGPTEKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIFKKLKSNSKEIECDLLKWSTNKSESHLLVSSSLKDYSIYLWNVRDEKLIVKFSKSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSGYYMIGKGSFSSRYSPELLADVLYQKNPFEWDTFYDKTKLVESINSSIREVEVHYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IELY ISNNVKDIETKDIRISIMEKAEKEVNEMFGTTNPDYGWKIYLKKLDMEILIKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:44689"
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                                                                                                                                                                              LIFQSIMEPGLIGKSVQLHAEYSHIISCKYLFDKSEWLAHFSKDWYKEQRYIKDKINK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Dictyostelium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .892,1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al protein"
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codon_start=1

CDS

CDS

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TTITNRSLSTPILPSQVSNEPKSNGRKKRKKDT
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NNNNSNSNIDIKSLPPYQRGGIAIQTKSIELLKFKSLNKSMIEPEIIDFDFMKDSRYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLIRHSIEIFKERNENQLPREFNKDDSMEFVKIVNEFNMNDYFKFDHLNDDQIKEDQL
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DQKLNRAIISQSHLQELNPYVKVNTTTNLSLSDLILNNSNSLLQFKCIILTESNLNDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(11969. .12112)
/note="ORF_ID:dd_01752"
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AAFNLDRVLSGKNHSNS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAM33691.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="TRANSCRIPTION FACTOR DP1. 6/101"
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/note="ORF_ID:dd_03277"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {	t RNLATLEAILKPVEEGGLVANSLVFRYNLTHGHDDHIATDGLDGEEGTFNICTFWLIE}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {	t SKIMCWVALDRGLRLADRRSFPAPRDKWTKITQFYGSKALDASTLIMSLVFFMAPSDP}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRCAEAVYDDPKRSMPVRVMYSIHGDDKIPEYTLDHLSGYRDSKPVRVGNDAINQVQM
DIFGEFMDSIYLSNKYGSLVSYDFWLHIRKMVDWVADNYQTKDEGIWEVRSGKQHFTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKINEFCKENDIKFIVPDCYGLGGWVFNDFGDEFKVYDKNGEKLKEVFISNISISTQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="Putative Ligase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical 74.5 kDa protein"
                                                                                                                              .20984,21181.
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Matches
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
57840 AATTGTATGTTTTGATAAAACTTTTTCAACTTTTGGAGATTTACCAGAATTAT 57892
                                                                                            121 TTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATAT 173
                                                                                                                     99;
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFLYKFIDMKYIYIGGNLLQCIFFALFYFYESKIGSLLLIASTGIPWAIYMILPFSIY
GMGVEDNESSGLNIGTLNIFYVYPQMYVSLGIGLILDLSKGNVYYSLLTGSYASFFAT
LFCFRIIIPKHHGHPIGDIEEIHFNIENNNSGNKYSPWYKSDNNNNNNNNNNNNNNNNNNNNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILIGSVFISIGLVLISNAETFGSYFGDSEQKKSIAISIAIVGFWILDLSNNAVQAPCR
ALLVDIAAPSQQSLGSSLFSLMLGTGNLLGYMMGSIDLVRMVPFMKTDTRALFTLSIM
VLLFCVVMTLGFVTEEQYIRVNEDQSVENPLKTMFKGIVKMPTYLQRLCAVQFFSWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLKANEHAPKILSSYSISSSCGNPHHSETSTTPKQPMTTTTTTTTASTANSLSSLNTS
SSLGASSSGILNTSNENTPIIGGVLKIDNEILLNSGHKKTLPLFNLICLTICFLGVQF
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SYQVIQSQQSYSNY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WFSFVLFITTWVGVNVFGGDPNAPEYSDSRILFQDGVRWGSLSLTISSGITIAVSLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation-"MTYNNSNSKNKIKNKYYKQEDETINEDENDIKEEEEEEEEEKEEK
EGNINNNNNSNKINIEKDTNFIDKTNLGNGEGDSGGGGGDSGGCGGGGNDDGKEKKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="ORF_ID:dd_03122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=]
                                                                                                                                                                                                                                                                                                         15.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (22963.
                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                         Score 54.6; DB Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23481,23575. .23880,24038. .24268,24810. .24970,
                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                     74;
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                                                                                                                                                                                                                                                                                                                                  Length 123280;
                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                   Gaps
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                                                                                            57839
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Search completed: June 11, 2003, 01:50:13 Job time : 956.95 secs

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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0% Maximum Match 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Run on:
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                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                   Score
                                                   56.4
55.6
55
       100.0
16.2
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                                                                                                                                                                                                                              Match
                                                                                                                                                                                                                                                     Query
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358
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11:
12:
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SIDS2/gcgdata/geneseq/geneseqn-embl/NA198.DAT:*

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9837.455 Million cell updates/sec
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Human immune syste Human metastasis a Human immune syste DNA transcription
                                                                                      DNA encoding a cyt
Human immune syste
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Tumour suppressor
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Human gene regulat	AAS61123	24	6609	13.8	49.4
Chemically treated	ABL70526	24	6609	13.8	49.4
Human immune syste	ABL33926	24	13427	13.9	49.6
_	ABN80106	24	12639	13.9	49.6
	ABL32218	24	11422	13.9	49.6
chemically	ABK39936	24	11422	13.9	49.6
	ABL49336	24	9347	13.9	49.6
Human immune syste	ABL34175	24	113515	13.9	49.8
Chemically treated	ABL70544	24	15649	13.9	49.8
DNA transcription	ABK28280	24	8866	13.9	49.8
ally pretre	AAS45433	22	8866	13.9	49.8
	ABL32738	24	6759	13.9	49.8
	AAS46563	22	6134	13.9	49.8
r suppr	AAS46704	22	14615	14.0	50.2
Human immune syste	ABL33248	24	5163	14.1	50.4
Human immune syste	ABL32849	24	5649	14.1	50.6
Human chemically p	ABK40008	24	5649	14.1	50.6
Tumour suppressor	AAS46384	22	5649	14.1	50.6
DNA transcription	ABK28313	24	13606	14.2	50.8
Human immune syste	ABL33810	24	13606	14.2	50.8
Tumour suppressor	AAS46561	22	13606	14.2	50.8
	AAS45457	22	13606	14.2	50.8
	ABL32742	24	8087	14.2	50.8
immune	ABL33019	24	5311	14.2	50.8
immune	ABL32615	24	13584	14.2	51
immune	ABL33053	24	17131	14.4	51.6
immune	ABL32972	24	6145	14.5	51.8
₩	ABL32521	24	16750	14.6	52.2
Tumour suppressor	AAS46314	22	16750	14.6	52.2
Human gene regulat	\mathbf{L}	24	6418	14.6	52.2
Human immune syste	ABL32322	24	6418	14.6	52.2
hila melano	ABL19002	23	21231	14.7	52.6
-	ABL33138	24	5678	14.7	52.8
suppressor	AAS46670	22	7261	14.8	53
	339	24	14147	14.9	53.2
Tumour suppressor	74	22	14147	14.9	ü.

ALIGNMENTS

RESULT 1
AAAA59599
ID AAAA59599;
XX
AC AAA59599;
XX
DT 14-NOV-2000 (first entry)
XX
DE DNA encoding a cytochrome P450 enzyme designated DWF4.
XX
DWF4; cytochrome P450 enzyme; brassinosteroid; 22alpha-hydroxylation;
XX
CN
KW
Plant phenotype; cell elongation; ss.
XX
OS
Arabidopsis sp.
XX
FT promoter 1.3203
FT SATA_signal 3060.3125
FT CDS 3203.3125
FT exon 3203.3423
FT exon 3203.3423
FT exon 3203.3423
FT intron 3424.3828
FT intron 3424.3828
FT intron 3829.3913
FT intron 3829.3913

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                                                                                                                                 Query Match
Best Local
                                                                                                Matches
                                                                                                                                                       The present sequence encodes à DWF4 polypeptide. The polypeptide is a cytochrome P450 enzyme that mediates multiple steps in synthesis of brassinosteroids. Specifically, it mediates multiple 22alpha-hydroxylation steps in brassinosteroid biosynthesis. The DWF4 polynucleotide is used for altering the phenotype of a plant. DWF4 plants display a dramatic reduction in the length of different organs, and this size reduction is attributable to a defect in cell elongation. The DWF4 polynucleotides and polypeptides can be used in diagnostic assays and to generate antibodies, which can be used to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
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                                                                                                                                 Sequence 6888 BP;
                                                                                                                                                                                                                                          Claim 3; Fig 10A-G; 113pp; English.
                                                                                                                                                                                                                                                             plants,
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11-FEB-1999;
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                                                                                                                                                immunogenic compositions.
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                                                             6111
                                                                                                                                                                                                                                                          isolated dwf4 polynucleotide useful for altering the phenotype of its, for diagnostic assays and in the production of antibodies -
           121
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)B; AAB07921.
                                            61
                                                                                                358;
                                                                                                       Similarity
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TTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGG
                                                          Conservative
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99US-0119658
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                                                                                                      Score 358;
Pred. No. 3.
                                                                                              Mismatches
                                                                                                      DB 21;
3.2e-55;
                                                                                                                                2391 T;
                                                                                                                                0 other;
                                                                                              Indels
                                                                                                              Length 6888,
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                                                                                             Gaps
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Matches Query Match Best Local

85;

Conservative

0;

Score 58; DB Pred. No. 0.05 0; Mismatches

.053;

45;

0

Gaps

0

63

Similarity

16.2%;

Sequence

5449

BP;

1146 A; 90 C; 1299 G;

2914 T;

0 other; Length 5449; Indels

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RESULT 2
ABL33641
ID ABL33
XX ABL3
XX ABL3
XX ABL3
XX ABL3
XX ABL3
XX Huma
XX Huma
XX Huma
XX Huma
XX Huma
XX Homo
XX ABL3
XX ABL3
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XX ABL3
XX Huma
XX Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antirheumatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                         genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                  present invention provides a number of human immune system associated es which are modified by the methylation of cytosines. The sequences
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                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1614; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                             methylation
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2000DE-1043826
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Matches 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; antiarthritic; antidiabetic; antipartic; antiarthritic; antidiabetic; antisporiatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL33223;
                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                            macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilosy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002
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for diagnosis and treatment
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                                                                                                    159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune system disease; cytosine methylation; antiasthmatic;
                                                   N
                                                                                                                         Similarity
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7560 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piepenbrock C,
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                                                                                                                                                                                                 2154 A; 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133
                                                                                                                   16.2%;
51.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragment of chemically modified ment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berlin
                                                                                               Pred. No. 0.0
0; Mismatches
                                                                                                                                                                                                 ç
                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arthritis; psoriasis;
                                                                                                                                                                                                 1554 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ζ,
                                                                                                                                           58;
                                                                                            DB 24; 0.053; ches 145;
                                                                                                                                                                                                 3805
                                                                                                                                                                                                 ₽.
                                                                                                                                           Length 7560;
                                                                                                                                                                                                 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene, useful abnormal
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                              Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation \,
                                                                                                                                                                                                                                           Olek
                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL33652
                                  macular degeneration, arteriosclerosis, anaemia, cancer, acute my leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                       can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                The present invention provides a number of human immune system associat genes which are modified by the methylation of cytosines. The sequences
                                                                                                                                      Claim 1;
                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                           30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                 02-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                          03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                   WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                   gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
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                                                                                                                                                                                                                                                                   (EPIG-)
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                                                                                                                                                                                                                  2002-130909/17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune
                                                                                                                                                                                                                                                                   EPIGENOMICS
                                                                                                                                        SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACAACTT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCTAGGTTGAGTCTTTGGACATTTGTATTTGGATGT----TGTTGATTATTAGTGTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATTATTAAATTAATTTGATAAATAGTAATAAATGTGTGATGTATGTTATTTTAAATTT
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                                                                                                                                                                                                                                          Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTTTTGCCCCAATGATATAAAAATTTGGATAATAATATTATTGGATATTCGTTTTT 121
                                                                                                                                        ID NO 1625;
                                                                                                                                                                                                                                                                                           2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 system associated
                                                                                                                                                                                                                                                                                                                                 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         system disease; cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3035
                                                                                                                                                                                                                                                                                                                                                                                                                                                  rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
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                                                                                                                                      32pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiasthmatic;
                                                                                                                                                                             gene, us
                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease,
                                                                                                                associated
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Sequence 5926

BP;

1562 A;

55

C; 1318 G;

2991 T;

0 other

the invention

acute myeloid

diseases. The present sequence is a gene of

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RESULT 5
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                                                                                                                                                                                                     15-MAR-2000;
06-APR-2000;
07-APR-2000;
 The invention relates to a nucleic acid comprising a bases, of a segment of chemically pretreated DNA (CP
                                                                             Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for
                                                                                                                                       01ek
                                 Claim 1; SEQ ID No 232; 27pp; English.
                                                                   analysing
                                                                                                                                                                                  30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                  Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism
                                                                                                                                                                                                                                                  15-MAR-2001; 2001WO-EP02955
                                                                                                                                                                                                                                                                                               WO200168912-A2
                                                                                                                                                                                                                                                                                                                                          cytosine
                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS46510 standard; DNA; 12356
                                                                                                                                                             (EPIG-)
                                                                                                                                                                                                                                                                          20-SEP-2001
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                                                                                                                                       ۶,
                                                                                                                2001-602752/68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                    suppressor gene derived chemically modified sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                             EPIGENOMICS
                                                                                                                                       Piepenbrock
                                                                                                                                                                                                                                                                                                                                          methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTAGGTTGAGTCTTTGGACATTTGTATTGGATGTTGATTATTAGTGTCGACACTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATGAGATATTAAGTTTTAGGAAGAAGAAGAGATTTTGGAATGGAAATATTTTTGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTTTGCCCAATGATATATAAAAATTTGGATAAATAATAATATTGGATATTCGTTTTTTA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAACCTTAAATGGGCTTTCTATAAGGCCCCAATTATATTACGATTATAACAAAGTGACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTTACTTCGTTTTTGATCCGAAGCAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTAACGAAAGTTGGGTTGGAGGATTGGGTAGGTAGCGTTGGAAAGTATGTTAGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATATTTGATTTTTGAATGTATTTAATAA 3500
                                                              ourcogenes, useful in designing primers diseases associated with cytosine methy
                                                                                                                                                                               2000DE-1013847.
2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                           ĄG
                                                                                                                                                                                                                                                                                                                                                 dinucleotide; single-nucleotide polymorphism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.8%;
                                                                                                                                       Berlin
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Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 333
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                                                                  imers and probes for
methylation state e
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sequence c
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                                                                                                                                                                                                                                                                                                                                                                                    #232
  of 18
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC bisulphite, of genes associated with tumour suppression and CC oncogenes having a sequence taken from 536 (actually 533 since CC numbers 408, 458 and 500 are missing from the sequence listing) sequences CC (SS) and sequences complementary to (SS). The nucleic acid may be a CC form part of a set of probes for detecting the cytosine methylation state CC and/or single nucleotide polymorphisms and also to be used in an CC array for analysing diseases associated with CpG dinucleotides e.g. CC concers and tumours. The probes can also be used in a method for CC ascertaining genetic and/or epigenetic parameters for the diagnosis CC diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters which are disadvantageous to patients. The present sequence is one of the CC are disadvantageous to patients. The present sequence is one of the CC complementary sequence of the corresponding odd numbered sequence (e.g. CC IS missing).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 118
                                                                                                                      neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arterioscierosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
                                                                                                                                                                                   antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                          Homo sapiens.
                                                                                                         gene;
                                                                                                                                                                                                                  Human; immune system disease; cytosine methylation; antiasthmatic
                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                                                                                                АВL32028;
                                                                                                                                                                                                                                                                                                                                               ABL32028 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12356 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ls missing)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9051
                                                                                                                                                                                                                                                                                                                                                                                                                          9231 ATTTTATTGTAGTTTTGATTTGTATTTTTTTGATGATTAATG 9272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity
118; Conserv
                                                                                                                                                                                                                                                    immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGATTATATGGTAGTTTAATTTTTAGTTTTTGAGGAATTTTTAAATTGTTTTTATAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGTCTTTGGACATTTGTATTGGATGTTGTTGATTATTAGTG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                  system associated
                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3645 A; 68 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.5%;
53.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2127 G;
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0.14;
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                                                                                                                           disease;
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WO200200928-A2

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RESULT 7
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Best Local S
Matches 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, theumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EPIG-)
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01-SEP-2000;
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                                                                                                                                     Human metastasis
                                                                                                                                                                                                                                                       ABL34611 standard;
     W0200177376-A2
                                                                               cytosine methylation;
                                                                                               Metastasis associated
                                                                                                                                                                             26-MAR-2002
                                                                                                                                                                                                                   ABL34611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention provides a number of human immune es which are modified by the methylation of cytosines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             methylation
                                                                                                                                                                                                                                                                                                                                                     TTTAATAAGAATGTAAAATTTTTAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                         ATCCGAAGCAATAACAAATTGTCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                            TTCTATAAGGCCCAATTATATTACGATTATAACAAAGTGACAACTTTTACTTCGTTTTTG
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2000DE-1043826
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Pred. No. 0.18;
0; Mismatches
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                                                                               cytostatic;
                                                                                                                                     gene
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                                                                                             therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 7351;
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abnormal
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 RESULT 8
ABL34127
ID ABL3
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HUMBA
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                                                                                                                                                                                                                                                                                                                                 日
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Matches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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30-JUN-2000;
01-SEP-2000;
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antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20486 BP; 6101 A; 360 C; 4446 G; 9577 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of human metastasis associated which are modified by cytosine methylation. The sequences can used in the diagnosis and treatment of cancer. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 164; 23pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           also for treatment
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                                                                           Human;
                                                                                                                 Human
                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                   ABL34127 standard;
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                                                                                                                                                                                             ABL34127;
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                                                                                                               immune system associated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 ATATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTAGTTCGGGTTTGAG
                                                                         immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for diagnosis of cancers by analysis of cytosine methylation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piepenbrock
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
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49.6%;
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RESULT 9
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Best Local S
Matches 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic
for diag
            DNA transcription
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                                     23-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                     ABK28455 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases. The present sequence is a gene of the invention.
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acute myeloid leukaemia; Alzheimer's disease; AIDS;
neurofibromatosis; rheumatoid arthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leic acid comprising fragment of chemically modified gene, useful diagnosis and treatment of diseases associated with abnormal
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                                                                                                                                                                                                   183
                                                                                                                                                                                                                                                                          140
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                                                                                                                                                                                                                                                                                                                                                                                                    146;
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                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                  GACATTTGTATTGGATGTTGATTATTAGTGTCGACACTATTAAACCTTAAATGGGCT 259
                                                                                                                                                                                                                                                                         AGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTTGAGTCTTTG 199
                                                                                                                                                                                                                                                                                                                                                                2814 BP; 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piepenbrock C,
                                                                                                                                                                       TTCTATAAGGCCCAATTATATTACGATTATAACAAAGTGACAACTTTTACTTCGTTTTT 318
                                                                                                                                                                                                                                                                                                 TACGTGTAGGTGGATATATTTTTTTGTATATTTTCGTGTATATGTAAATTTTTTTGTAT 122
                                                                                                                                                                                                                                                                                                                         TATAAAAATTTGGATAAATAATTATTGGATATTCGTTTTTTAGTTCGGGTTTGAGAAA 139
                                                                                                                                                                                                                                                                                                                                                ATGTATATGTTATATATATGTTATGTGTGTGTATATACGTTTTTTGTATAAACGTTTATA
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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2000DE-1043826
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                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ID NO 2100;
            associated
                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AG
                                                                                                                                                                                                                                                                                                                                                                                                             15.1%;
48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; 144 C;
                                                                                      7138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berlin
                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 54.2;
Pred. No. 0.
           genomic DNA #165
                                                                                      ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                         DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                 153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 other;
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bowel disease;
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63

TTTTTGAGATATGTTTATTTTTTTTTTTTTTTT

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TTTTTTGCCCAATGATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTT 122

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3163

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Query Match Best Local Matches

Loca l

Similarity

15.1%;

153;

Conservative

0;

Score 54; DB 24 Pred. No. 0.27; 0; Mismatches 1

Length 7138; 0 other

Indels

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Gaps

Sequence

7138

BP;

1564 A;

288 C;

1759 G;

3527 T; 24; 165;

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CC chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer, in particular an oligonucleotide cor peptide nucleic acid (PNA)-oligomer that hybridises to or is identical to the chemically pretreated DNA of genes associated with DNA cranscription. The set of oligomer probes are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for despecting the cytosine methylation state associated with DNA transcription (particularly with the methylation status), e.g. adenosine deaminase deficiency, viral infection, retroviral infection, Sezary syndrome, tuberculosis, developmental disorders, psoriasis, Rieger's syndrome, ctuberculosis, developmental disorders, psoriasis, Rieger's syndrome, neurodegenerative disorders, Waardenburg syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial cyndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial cor cancer. Sequence arthritis, polyglutamine disorders, solid tumours or cancer. Sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from the current of fire.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA transcription associated gene; peptide nucleic acid; PNA-oligomer; PNA; cytosine methylation state; SNP; retroviral infection; gene; ds; single nucleotide polymorphism; adenosine deaminase deficiency; cancer; viral infection; Sezary syndrome; haematological disorder; tuberculosis; immunological disorder; Werner syndrome; developmental disorder; psoriasis; Rieger's syndrome; neurological disorder; erythropolesis; neurodegenerative disorder; Wardenburg syndrome; Niemann-Pick disease; myelodysplastic syndrome; myocardial infarction; hypertension; arthritiangiogenesis; congenital heart disease; HDR syndrome; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, sol
European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a nucleic acid, which comprises a segment of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
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30-JUN-2000;
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    Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID No 329;
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2000DE-1043826.
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              The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CPG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-APR-2000;
07-APR-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 467; 27pp; English
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cancer; tumour; CpG dinucleotide; single-nucleotide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of chemically modified genes associated with tumour oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state
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; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to pattents. The present sequence is one of the 533 genomic sequences derived from tumour suppressor genes and
                                           01ek
                                                                                      30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                              Human; ds; astrocytoma; cytostatic; staging; cysteine methylation; bisulphite; brain tissue; MALDI; ESI; electron spray mass spectrometry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14147 BP;
                                                                                                                       02-JUL-2001; 2001WO-EP07538
                                                                                                                                                                   WO200202808-A2
                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                       ABK33955
                                                                                                                                                                                                                                                                                                                              ABK33955
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                                                                 (EPIG-)
                                                                                                                                             10-JAN-2002.
                                                                                                                                                                                                                                                                                 18-JUN-2002
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                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 AAAAAGATGAAAGTATTTTATTCTCTTCTTTTTTTTTTGATAATTTTAAATCATTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                 EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock
                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                   TTATTATTATTTGA 11124
                                                                                                                                                                                                                                                                                                                                                                                                          TACTTCGTTTTTGA 320
                                                                                                                                                                                                                                                                                                                                                                                                                               CCTTAAATGGGCTTTCTATAAGGCCCAATTATATTACGATTATAACAAAGTGACAACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACTATTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGCCCCAATGATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTT 126
                                                                                                                                                                                                                                                          for staging of Astrocytomas #20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                      2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3621 A; 225 C;
                                                                                                                                                                                                                                                                                                                            DNA; 14147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.9%;
                                          Ç
                                           Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53.2; DB Pred. No. 0.36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                           <u>~</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7185 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 14147;
                                                                                                                                                                                                                        nylation; CpG, spectrometry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Novel chemically modified genomic DNA sequences, useful in

WPI; 2002-171649/22

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CC for determining generic and/or epigenetic parameters, classification, CC differentiation, grading, staging, treatment and/or diagnosis of CC astrocytomas, or the predisposition to astrocytomas by analysing cytosine methylations, involves obtaining a biological sample containing genomic CC methylations, involves obtaining a biological sample containing genomic CC DNA, extracting the genomic DNA, converting cytosine bases which are CC unmethylated at the 5-position, in the genomic DNA sample, to uracil or CC denoter base which is dissimilar to cytosine in terms of hybridisation of CC denoter base which is dissimilar to cytosine positions by reference to complificates carry a detectable label. The method further involves cone or more data sets. The genomic DNA is chemically treated by using a bisulphite, hydrogen sulphite or disulphite. The amplificates carry a contribution of particular interest in astrocytoma or constraintissue, based on the specific genomic methylation status of brain tissue, based on the specific genomic methylation status of brain curves, as opposed to background DNA. The amplificates carry a constraintissue, as opposed to background DNA. The amplificates carry a constraintissue, based on the specific genomic methylation status of brain curves. As opposed to background DNA. The amplificates carry a constraintist of the cytonally, the labels of the constraintist are detected in a mass spectrometer. The fragments of chemically pre-treated genomic DNA to be amplified, have a single positive or negative charge for a better detectability in the mass spectrometer. The fragments of chemically pre-treated by matrix assisted laser desorption/ionization mass spectrometery (MALDI) or using electron spray mass spectrometry (ESI). The constraint of the chemically pre-treated reference DNA constraints of the chemically pre-treated reference DNA constraints of the chemically pre-treated reference DNA constraints. But was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the printed specification, but was format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14147 BP; 3621 A; 225 C; 3116 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTTTTCGAATTTATGTTAGTTTTTTTTTTTTTATGTTATTTTAGGTATTTTTAGTT
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48.1%;
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
                                                                                                                                                                                                                          Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g. cancer
                                                                                                                                                                                                                                                                           Olek A,
                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                        01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                           cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                  Human; tumour suppressor gene; one cancer; tumour; CpG dinucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumour suppressor gene derived chemically modified sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS46670
                                                                                                                                                                                                                                                                                                                                                  15-MAR-2001; 2001WO-EP02955
                                                                                                                                                                                                                                                                                                                                                                               WO200168912-A2
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                         (EPIG-)
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                                                                                                                                                                                                                                                                                         EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; DNA; 7261 BP
                                                                                                                                                                                                           SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACTTCGTTTTTGA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTATTATTATTTGA 11124
                                                                                                                                                                                                                                                                                                      2000DE-1013847.
2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                                          392; 27pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                         oncogene;
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                                                                                                                                                                                                                                                                                                                                                                                                                  single-nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                         antitumour;
                                                                                                                                                                                                                                                                                                                                                                                                                  polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                         #392
                                                                                                                                                                                                                                                                                                                                                                                                                   SNP;
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CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CC bisulphite, of genes associated with tumour suppression and CC oncogenes having a sequence taken from 536 (actually 533 since CC numbers 408, 458 and 500 are missing from the sequence listing) sequences CC (Ss) and sequences complementary to (Ss). The nucleic acid may be a CC peptide nucleic acid-oilogner (PNA) of at least 9 nucleotides and may CC form part of a set of probes for detecting the cytosine methylation state CC and/or single nucleotide polymorphisms and also to be used in an CC array for analysing diseases associated with CpG dinucleotides e.g. CC cancers and tumours. The probes can also be used in a method for CC arcertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific CC and/or therapy of existing diseases or the predisposition to specific CC diseases, by analysing cytosine methylations. The parameters may be CC compared to another set of genetic and/or epigenetic parameters the CC differences serving as basis for diagnosis and/or prognosis events which CC are disadvantageous to patients. The present sequence is one of the The invention relates to a nucleic acid comprising a sequence bases, of a segment of chemically pretreated DNA (CP DNA) e.g. of 18 with sequences state

533 genomic sequences derived from tumour suppressor genes and oncogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence ID 2 and ID1, ID 536 and ID 535, except for those whose partner is missing) patent did not form ID numbers are the odd numbered sequence (e.g. those whose partner sequence

Note: The sequence data for this post the printed specification, but format directly from WIPO at was obtained in electronic

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL33138 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                 30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                               gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL33138
                                                          Claim
                                                                                          Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                           (EPIG-)
                                                                                                                                                                                                                                   02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                           03-JAN-2002
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                                                                                                                             2002-130909/17.
                                                                                                                                                                                                                                                                                                        sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    immune
                                                                                                                                                                                                                                                                                                                                                                                                             immune system disease;
                                                                                                                                                                           EPIGENOMICS
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                                                                                 methylation
                                                                                                                                                   Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGGCTTTCTAT
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                                                          NO 1111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                             cytosine methylation; antiasthmatic;
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                                                        Sequence Listing;
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3, 0.41;
3-ches 125; Indels
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neovascular glaucoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 7261;
                                                          German
                                                                                                                                                                                                                                                                                                                                        epilepsy;
bowel dis
                                                                                          gene, useful
abnormal
                                                                                                                                                                                                                                                                                                                                                              anaemia;
                                                                                                                                                                                                                                                                                                                                          disease;
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                    capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukarytes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL10176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
            sequences (ABL01840 (ABB57737-ABB72072)
                                                                                           The invention relates to an isolated nucleic acid detection reagent
                                                                                                                Claim 1; SEQ ID NO 8479; 21pp + Sequence Listing; English
                                                                                                                                                  New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                            Venter
                                                                                                                                        interactions
                                                                                                                                                 from Drosophila
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SSSSXX
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           macular degeneration, arteriosclerosis, anaemia, cancer, acute my leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
WPI; 2001-656860/75.
                                                                                                                      23-MAR-2001;
                                                                                                                                                27-SEP-2001.
                                                                                                                                                                            WO200171042-A2
                                                                                                                                                                                                      Drosophila melanogaster
                                                                                                                                                                                                                               pharmaceutical;
                                                                                                                                                                                                                                                                        Drosophila melanogaster genomic polynucleotide SEQ
                                                                                                                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                                                                                                              ABL19002;
                                                                                                                                                                                                                                                                                                                                                       ABL19002 standard;
                                                  (PEKE ) PE CORP NY.
                                                                               11-JUL-2000;
                                                                                           23-MAR-2000;
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                                                                                                                                                                                                                                             developmental
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                                                                             2000US-191637P
2000US-0614150
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                                                                                                                      2001WO-US09231.
                                                                                                                                                                                                                               gene;
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                                                                                                                                                                                                                                                                                                                                                         DNA;
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54.0%;
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                          PWD,
                                                                                                                                                                                                                                             biology; cell signalling;
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                                                                                                                                                                                                                                                                                                                                                      ВP
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for this patent did not form part of the printed

detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel

cell-cell

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ABL32322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antilarbridge antilarbridge antilabetic; antipsoriatic; antilarbridge antilarbridge antilarbridge antilarbridge antilarbridge antilarbridge anteriosclerosis; anaemia; antilarbridge acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
cytosine
                                                                                                                                                          Olek A,
                                                                                                                                                                                                                                                              30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; immune system disease; cytosine methylation; antiasthmatic;
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                  Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                          02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                             (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human 1mmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL32322 standard; DNA; 6418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21231 BP; 6727 A; 3859 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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  methylation
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                                                                                                                                                                                                                                                              2000DE-1032529
2000DE-1043826
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46.8%;
                                                                                                                                                          Berlin
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                                                                                                                                                          <u>.</u>
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                     abnormal
                                                gene, useful
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Best Local :
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                                                                                                                                                                                                                                                        The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                 Sequence 6418 BP; 1842 A; 47 C; 1423 G; 3106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
1230
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                           138
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                                                                                                                                           18
                                                                                                                                                                                       Similarity
                                                                                                                             TAATTGGATTTATTTTTTTTAGGGGATAATTTATTATGGTTTTTATTTA
                AAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTA
                                                        TATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTTCGGGTTTGAGA
                                                                                                              SEQ ID NO 295;
                                                                                                                                                                          Conservative
                                                                                                                                                                                       14.6%;
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                                                                                                                                                                                       Score 52.2; DB Pred. No. 0.57;
                                                                                                                                                                        Mismatches
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Search completed: June 10, 2003, 22:22:49
Job time: 83.9537 secs

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Title:
Perfect score:
Sequence:
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No.
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Maximum DB seq
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                          Score
                       386.22
86.22
                                                                                                                 Issued_Patents_NA:*

1: /cgn2_6/ptodata/1

2: /gn2_6/ptodata/1

3: /cgn2_6/ptodata/1

4: /cgn2_6/ptodata/1

5: /gn2_6/ptodata/1

6: /cgn2_6/ptodata/1
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length: 2000000000
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(without alignments)
6438.831 Million cell updates/sec
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358
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Gapop 10.0 , Gapext 1.0
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    Copyright
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                          Length
   GenCore version 5.1.6 (c) 1993 - 2003 Compugen
                                                                                                                                                                                                                                                                                          DB
                        US-08-078-090-3
US-08-341-568-3
US-08-911-020-3
US-08-911-020-3
US-08-447-8268-13
US-09-410-464-1
US-08-998-416-547
US-08-998-416-498
US-07-867-106-4
US-08-998-416-26
US-09-005-051-26
US-09-134-0010-2606
US-09-134-0010-2606
                                                                                                                                                                                              US-08-340-820-24

US-08-593-535-24

US-09-122-400B-5

US-08-378-313-24

US-09-056-075-1

PCT-US2-06300-1

US-09-073-569-1

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Sequence 24, Appl
Sequence 24, Appl
Sequence 5, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 4, Appli
Sequence 44, Appli
Sequence 44, Appli
Sequence 44, Appli
Sequence 26, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 28, Appli
Sequence 26, Appli
Sequence 27, Appli
Sequence 26, Appli
Sequence 27, Appli
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RESULT 1 US-08-340-820- US-08-340-820- Sequence 24, Patent No. 5 Patent No. 5 Patent No. 5 REGENERAL INH REPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT APPLICANT TITLE OF TITLE OF TITLE OF CORRESPON ADDRESS ATTILE APPLICA FILING FILING FILING FILING ANTICHEN TELEFH TIPE: REGISTANDE TOPOLOG MOLECULE ANTI-SENA ORIGINAL ORGANIS	00000 00000000000000000000000000000000
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JS/08340820 -ichi ako resutomu suya suya suya suya contin; DIKE, contin; DIKE, creet disk npatible -Dos/MS-Dos Palease #1.0, v Pa: US/07/835,713	2555 2 US-08-693-457-3 2555 4 US-09-265-731-3 2555 4 US-09-265-731-3 2555 4 US-09-265-731-3 2556 2 US-08-392-625-16 2570 2 US-08-445-1938-1 2582 3 US-08-545-1968-1 2571 4 US-09-180-852-1 25852 1 US-07-867-106-4 25852 1 US-07-867-106-2 2574 4 US-08-897-534A-8 2574 4 US-08-897-534A-8 25759-9-1 2674 4 US-08-897-534A-8 25759-9-1 2674 4 US-08-897-344-26 2745 6 521590-9 2746 6 521590-9 2747 6 US-08-897-344-8 2748 1 US-08-897-344-8 2749 A US-08-897-344-26
FACTOR AND ITS BRONSTEIN, ROBERTS &	_ N0&6
	Sequence 3, Appli Sequence 16, Appl Sequence 16, Appl Sequence 18, Appl Sequence 18, Appl Sequence 11, Appl Sequence 1, Appli Sequence 5, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 73, Appli Sequence 73, Appli

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; IMMEDIATE SOURCE:
; LIBRARY: Human foreskin cDNA library
; CLONE: pGAF1
US-08-340-820-24
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US-08-593-535-24/c
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                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-5440
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity Matches 77; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/835,713
FILLING DATE: 12-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, David G.
                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/593,535
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND TITLE OF INVENTION: PRODUCTION NUMBER OF SEQUENCES: 27
                        MOLECULE TYPE:
         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                       TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0: FILING DATE: 24-JAN-1996
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TISSUE TYPE: SKII
TYPE: fibroblast
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                                                                                       LENGTH:
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                                                                                    1493 base pairs
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KONDO, Tatsuya
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SEKO, Chisako
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                           CDNA to mRNA
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                                                                                                                                                                                                                                                                                                                                                            Version #1.25
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US-08-593-535-24
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                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09122400B Patent No. 6245974
                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: Michalowski and Spiker CURRENT APPLICATION NUMBER: US/09/122,400B CURRENT FILING DATE: 1998-07-24 PRIOR APPLICATION NUMBER: 60/066,118 PRIOR FILING DATE: 1997-08-06 NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Spiker, Steven
TITLE OF INVENTION: MATRIX ATTACHMENT REGIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                             LENGTH: 998
TYPE: DNA
ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
LIBRARY: Human foreskin cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE TYPE: skin
CELL TYPE: fibroblast
                                                                                                                                                                                                                                          Local Similarity
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439
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                                                                                  125 TTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGC 184
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                                                                                                                                         65 TTTTGCCCCAATGATATAAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAG 124
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TCAGCTTCTTTTTTTCAGTTTTTA 415
                          TAGGTTGAGTCTTTGGACATTTGTA 209
                                                                                                                                                                                                                                                                                                                                                        PatentIn Ver. 2.1
                                                       TTCAGTTTTTAGTAGTTTTTTCCAGATTTTACAAATAAAATTGCTTTAGAAAATTGATTT 440
                                                                                                                                                                     Michalowski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGGTTTCGACTTT
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57.5%;
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Pred. No. 1.
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                                                                                                                                                                                                                             Mismatches
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US-08-378-313-24/c

Sequence 24, Application US/08378313 Patent No. 6207881

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: THEOLOGIS
APPLICANT: SATO, TAK
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
PRIOR APPLICATION UMBER: US 07/862,493
FILING DATE: 02-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 856-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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STATE: California
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                            TTTGCATTCATTAATTAGCTAAGACAAATTATGATGTCTAAGTAC 1878
                                                        TTTTACTTCGTTTTTGATCCGAAGCAATAACAAATTGTCAAATAC 348
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GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
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Pred. No.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                  183 GCTAGGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACTAT 242
303. CTTTTACTTCGTTTTTGATCCGAAGCAA 330
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                                                                                                                                                                                                                          64 TITTTGCCCAATGATATATAAAAATTTGGATA-AATAATATTATTGGATATTCGTTTTTT 122
                                                                                                                                                                                                                                                                                                n 11.4%; Score 40.8; D
Similarity 47.3%; Pred. No. 2.3;
55; Conservative 0; Mismatches
                                                        TABACCTTABATGGGCTTTCTATAAGGCCCAATTATATTACGATTATAACAAAGTGACAA 302
                                                                                       AGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGA 182
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Bradshaw, Marite
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INFORMATION FOR SEQ ID NO: 1:
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CURRENT APPLICATION DATA:
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                                                                                                                                                              PAGES: U. 1986
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TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Similarity 52.3%;
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MOLECUILAR STRUCTURE OF THE HUMAN ALBUMIN GENE
IS REVEALED BY NUCLEOTIDE SEQUENCE WITHIN Q11-22
OF CHROMOSOME 4
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                                                                                                                                                                                   6747-6757
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Dennison, O E
Hawkins, J W
Beattie, W G
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Ruffner, D E
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Pred. No. 2.3;
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Best Local S
Matches 76
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Patent No. 6084088
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LENGTH: 1733 base pairs
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                                                                                                                                                                                        Local Similarity 56.: hes 76; Conservative
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SOFTWARE: FastSEQ for Windows Version
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                      AGGGTTTCGACTTTC 154
                                                              TATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTTCGGGTTTGAGAAA 139
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; APPLICANT: DZIEGIEL, MORTEN;BORRE, MARTIN;JEPSEN, SOREN;
; VUUST, JENS;RIENECK, KLAUS;WIND, ANNETTE;JAKOBSEN, PALLE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DK92/00236
FILING DATE: 19-AUG-1992
                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19930618
              SEQUENCE CHARACTERISTICS
                                                   TELEPHONE: (202)628-5197
TELEPHONE: (202)737-3528
                                                                                                                             APPLICATION NUMBER: WO PCT/DK91/00233
FILING DATE: 19-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                     RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy, disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT:
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                                                                                                      NAME: COOPER, IVER P. REGISTRATION NUMBER:
                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
ZIP: 20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 18-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2784 TTATATATAAATACTGGATAAATATTTATGTATATATTTATAT 2826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 TTTTTGCCCCAATGATATATAAAAATTTGGATAAATAATATTAT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64;
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                                         248633
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                                                                                                                                                                                                                                                                                                                                                                             D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08078090
                                                                                                                                                                                                                                                                                                                                                                                                 419 SEVENTH STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                             STROEMQUIST, MATS
VERVION: HUMAN BETA-CASEIN PROCESS FOR PRODUCING
VENTION: IT AND USE THEREOF
                                                                                                                                                                                                                                                                                   PatentIn
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HJALMARSSON, KA
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                           SEQ ID NO:
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62.1%;
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                                                                                                 28,005
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                                                                                         BERGSTROM2
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Pred. No. 2
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                                                                                                                                                                                                                                                                            Version #1.25
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US-08-749-522-2
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                           Matches
                                      Query Match
Best Local
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                                                                                                                                   TYPE:
                                                                                                                                             LENGTH:
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; NAME/KEY:
; LOCATION:
; LOCATION:
US-08-078-090-3
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Best Local Similarity 56.9
74; Conservative
                                                                                                                                         TELEFAX: (414) 271-3552 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                  STATE: "...COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 53202-4497
COMPUTER READABLE FORM:
CONFUTTIN TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION: APPLICANT: John,
                                                                                                                                                                              REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 671
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5709
                                                                        TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Baker, Jean C.
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 411 East
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 10607 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1043 GTAGATTAGT 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 GGAGCTAGGT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 TTTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          923 ATTTATAGTATAGAAATGAGTATAAAAACTAGTATAATTAGTATTAGTATATATTAGTAT
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                                                                                                               : 2755 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                        411 East Wisconsin Avenue
       Conservative
                                                                                         linear
                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Join(4804..4854, 5720..5746, 6726..6746, 6845
..6886, 7991..8521, 9440..9445)
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                                                                        DNA (genomic)
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                  11.2%;
48.3%;
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56.9%;
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  Score 40; DB 3
Pred. No. 3.3;
0; Mismatches
       0
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Pred. No. 2.8;
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                 DB 3;
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    180;
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                            Length 2755;
  Indels
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Gaps
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TELEY: (/u.,
TELEY: 248345
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
TYDE: nucleic acid
TYDE: single
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US-08-341-568-3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/341,568
FILING DATE: 22-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                 ORIGINAL SOURCE:
                                    MOLECULE TYPE:
                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Mannanase enzymes, genes coding for them,
TITLE OF INVENTION: methods for isolating the genes, and methods for bleaching lighter of invention: pulps
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   ORGANISM:
                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                       NAME: Murphy Jr, Gerald M
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGTGTATATTTG--TACTATTATTCTATATAAATTGATAACCTTATAAAAGTATCTAAT 2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGAAGTAAAATTATTTAACAAATATATTTTGAAAAAATTGATAAAAATACTAAATGAGGTT 2225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGGGTTTGAGAAAAGGGTTTCGA-CTTTCGAAAGTGGACGATGTATATAGATTGGGAGC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTGCCCCAATGATATAAAAATTTGGATAAATATATTATTGGATATTCGTTTTTTAGT 125
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Viikari, Liisa
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Saloheimo, Anu
 Trichoderma
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US-08-911-020-3/c
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Matches
                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 22-NOV-1994
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                      TELEFAX: (703) 205-805
TELEX: '248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                     MOLECULE TYPE: c
ORIGINAL SOURCE:
ORGANISM: Tric
                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 28,977
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: 7033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Birch, St
STREET: PO Box 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: lignocellulosic pulps NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: methods for isolating the genes, and methods for bleachin
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                                                                                          STRAIN:
                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                     NAME: Murphy Jr, Gerald M REGISTRATION NUMBER: 28,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 13-AUG-1997
                                                                                                                                                                                                                                                                                          TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Falls Church
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Marjatta, Ranua
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Siika-aho, Matti
Viikari, Liisa
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                                                                                                           Trichoderma reesei
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                 Score 39.4; D
Pred. No. 4.3;
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Pred. No. 4.3;
Mismatches
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                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                  TELEFAX: (619) 235-0176 INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: BINDING DOMAINS TITLE OF INVENTION: AND PLASMODIUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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STATE: California
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                                                              TTTGCCCAATGATATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGT 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           620 Newport Center Drive
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Nowhort Center Drive 16th Floor
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BINDING DOMAINS FROM PLASMODIUM VIVAX

BINDING DOMAINS FROM PLASMODIUM VIVAX

AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
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; TYPE: DNA
; ORGANISM: Populus
US-09-410-464-1
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; TYPE: DNA
; ORGANISM: Brachydanio rerio (zebra fish)
US-09-444-336-7
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US-09-444-336-7/c
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                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Strauss et al.
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09410464 Patent No. 6395892
                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 7
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               Query Match
Best Local S
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                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/410,464
CURRENT FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: 09/287,700
EARLIER FILING DATE: 1999-04-06
EARLIER APPLICATION NUMBER: 60/080,851
EARLIER FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DNA Encoding Proteins That Inhibit Hsp70 Function FILE REFERENCE: HspBp DNA and Protein Sequences CURRENT APPLICATION NUMBER: US/09/444,336 CURRENT FILING DATE: 1999-11-19 EARLIER APPLICATION NUMBER: 60/109,351 EARLIER FILING DATE: 1998-11-20
                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Floral homeotic genes for manipulation of TITLE OF INVENTION: poplar and other plant species. FILE REFERENCE: 53375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Guerriero, Vincent APPLICANT: Raynes, Deborah A
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Score 39; DB Pred. No. 5.2; 0; Mismatches
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5.2;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
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'Cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
'Cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
'Cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-239-676-140
US-10-239-676-117
US-10-239-676-115
US-10-239-676-115
US-10-239-676-151
US-10-239-676-151
US-10-239-676-150
US-10-239-676-160
US-10-239-676-170
US-10-239-676-107
US-10-239-676-107
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US-10-239-676-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEW_PUB.seq:*
                        Sequence 165, App Sequence 117, App Sequence 117, App Sequence 118, App Sequence 118, App Sequence 151, App Sequence 170, App Sequence 170, App Sequence 160, App Sequence 23, App Sequence 23, App Sequence 107, App Sequence 107, App Sequence 107, App Sequence 31, App Sequence 31, App Sequence 31, App Sequence 41, App Sequence 401, App Sequence 102, App Sequence 102, App Sequence 102, App
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Sequence
Sequence
             02, App
12673, 1
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APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013,1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 165, A Publication No.
                                                                                                                                                                                                                                                                                                                                         DE 10043826.1
PRIOR FILING DATE:
2000-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
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DE 10019173.8
DE 10032529.7
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o. US20030082609A1
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43.2	43.2	43.2	43.4	43.4	43.4	43.4	43.4	43.4	43.6	43.6	43.6	43.6	43.6	43.8	43.8	43.8	44.	44.2	44.4	44.4	44.4	44.4	44.6	44.6	44.6
12.1	12.1	12.1	12.1	12.1	12.1	12.1	12.1	12.1	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.3	12.3	12.4	12.4	12.4	12.4	12.5	12.5	12.5
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US-10-028-072-345	US-10-198-846-2709	US-09-960-353-6539	US-10-239-676-103	US-10-239-676-101	US-10-239-676-111	US-10-239-676-90	US-10-239-676-169	US-09-918-995-7147	US-10-239-676-2	US-10-239-676-185	US-10-239-676-67	US-10-239-676-164	US-09-960-352-2919	US-09-770-444-759	US-09-960-352-3400	US-09-960-352-5094	US-10-239-676-108	US-10-239-676-130	US-10-239-676-86	US-10-239-676-6	US-10-239-676-196	US-10-239-676-61	Δ,	-10-239-676-	US-10-239-676-191
sequence 2709, Ap Sequence 345, App		sequence 103, App				169,	/14/,				104,	, KTK7 #		3400,		٠.	Sequence 100, App	100,	, 0	, <u>F</u>	sequence bi, Appl	ي ي	4 1))

ALIGNMENTS

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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (4649, 7634, 7657)
US-10-239-676-165
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; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 165
; LENGTH: 13606
                                     Query Match
Best Local Similarity 52.3
                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
2001-04-06
                                                       14.2%;
52.3%;
                                                    Score 50.8; DB Pred. No. 0.83;
                                            Mismatches
                                                             DB 9;
                                           102;
                                                            Length 13606;
                                         Indels
                                         0;
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; LOCATION: (3405, 3418)
US-10-239-676-140
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Best Local
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NUMBER OF SEQ ID NOS:
SEQ ID NO 140
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                                                                                                                                                                                                                                                                                              Matches
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DE 10019058 8
DE 10019173 8
DE 10032529 7
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CURRENT FILING DATE: 2002-09-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure LOCATION: (3266,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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2000-04-07
2000-06-30
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TTAGTTATTAATATGTTATTATTGTTAAA 7054
                           CTATAAGGCCCAATTATATTACGATTATA 290
                                                      GATTGTTTGAATATGAAAATTATTTTTTTAAATATTGTAATATTTTTAATATGAAATA 7025
                                                                                   CATTTGTATTGGATGTTGATTATTAGTGTCGACACTATTAAACCTTAAATGGGCTTT
                                                                                                                TATATTTATTATATAAGTTTTTGTTTTTAGAAATTTGTTAAATTTAGATTATATTTTTA
                                                                                                                                           GGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTTGAGTCTTTGGA 201
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49.1%;
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Pred. No. 1.2;
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; NAME/KEY: unsure
; LOCATION: (1927...1928, 1943, 1956, 1958, 1981)
US-10-239-676-117 ·
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SEQ ID NO 117
LENGTH: 11036
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity
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Publication No. US20030082609A1
ENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 10032529.7
                                                                                                                APPLICANT: BERLIN, Kurt TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene FILE REFERENCE: 5013.1003
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APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
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CURRENT FILING DATE: 2002-09-24
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OTHER INFORMATION:
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DE 10019173.8
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51.4%;
                                                                                                                                                                         Christian
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Pred. No. 1.6;
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RESULT 5
US-10-239-676-115
Sequence 115, Application US/10239676
Publication No. US20030082609A1
GENERAL INFORMATION:
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           2000-04-07
2000-06-30
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NUMBER OF SEQ ID NO 115
SEQ ID NO 115
LENGTH: 5951
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2000-09-01
NUMBER OF SEQ ID N
SEQ ID NO 36
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                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
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APPLICANT: PIEPENBROCK, Christian
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LOCATION: (4511)
                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
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TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
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PRIOR FILING DA
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2000-04-06
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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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TYPE: DNA
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Local Similarity 47.0%;
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                                                                                                      OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-239-676-198
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APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases
FILE REFERENCE: 5013.1003
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: P
DE 10019058 8
DE 10019173 8
DE 10032529 7
DE 10043826.1
                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
SEQ ID NO 198
LENGTH: 7823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 198, Application US/10239676 Publication No. US20030082609A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 153; Conserv
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Best Local
                                                         Query Match
Best Local
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2000-04-06
2000-04-07
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CURRENT FILING DATE: 2002-09-24
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                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                   TYPE: DNA
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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGGGCTTTCTATAAGGCCCAATTATATTACGATTATAACAAAGTGACAACTTTTACTTC 312
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                                                         13.5%;
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                                           Score 48.4; D
Pred. No. 2.1;
0; Mismatches
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Pred. No. 1
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                                                                        Length 7823;
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US-10-239-676-151
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SEQ ID NO 151
LENGTH: 6327
TYPE: DNA
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Best Local
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CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 1003529.7
DE 10043826.1
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TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OLEK, Alexander
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                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                             184
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                                                                                                                                                                                                                                                                                                 157;
                                                                                                                                                                                                                                              20 TATTITTATICTCTTCTTTTTTTTTGATAATCTTTTAAATCATTTTTTTGCCCAATGATA 79
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                                                                                                                                                                                                                                                                                                              Similarity
TTTCTATAAGGCCCAATTATTACGATTATAACAAAGTGACAACTTTTACTTCGTTTTT 318
                              GGACATTTGTATTGGATGTTGATTATTAGTGTCGACACTATTAAACCTTAAATGGGC 258
                                                                                              GGATATTTTAGTTTTATAGAGAGGGGTTGAATTTTTTAGGTGAGGTTTGTTAGTTAATA 4117
                                                                                                                             AGGGTTTCGACTTTCGAAAGTG-GACGATGTATATAGATTGGGAGCTAGGTTGAGTCTTT 198
                                                                                                                                                             TTTTACTTCGTTTTTGATCCGA 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIEPENBROCK, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/10239676 o. US20030082609A1
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                                                                                                                                                                                                                                                                                                            13.4%;
52.3%;
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                                                                                                                                                                                                                                                                                                            Score 48; DB 9; Length 6327; Pred. No. 2.4;
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                                                                                                                                                                                                                                                                                           135; Indels
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; NAME/KEY: unsure
; LOCATION: (76),(90)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 25-LIB3057-018-Q1-K1-G1
US-09-960-352-5785
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-239-676-170
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US-09-960-352-5785
                                                                                    NUMBER OF SEQ ID
SEQ ID NO 170
LENGTH: 5610
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SEQ ID NO 5785.
LENGTH: 516
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TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
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                                                                                                                                                                                                DE 10043826.1
PRIOR FILING DATE:
2000-04-06
                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2002-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, C
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                                 FEATURE:
                                                  ORGANISM: Artificial Sequence
                                                                       TYPE: DNA
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70; Conserv
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                                                                                                                          NOS: 228
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Pred. No. 1.
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SEQ ID NO 160
LENGTH: 9515
TYPE: DNA
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Best Local
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DE 10019058.8
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CURRENT FILING DATE: 2002-09-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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                                                                                                                                TTTTGCCCCAATGATATATAAAAATTTGGATAATAATATTATTGGATATTCGTTTTTTAG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTTGAGTCTTTG 199
TCGTTTTTTTTTTTTTCGTTTGTTTATATCGTTTTATATAATAATTG 1624
                                                  CGTTTTTCGGGGTTTTAGATGTAGTTTTTTTTTTTTCGAAGTTGGGTTTAGATTGTTCGG
                                                                    TTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGC
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PIEPENBROCK, Christian
                                                                                                                                                                                                                  Conservative
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Pred. No. 3.9;
                                                                                                                                                                                                                            Score 46.8;
Pred. No. 4
                                                                                                                                                                                                                 Mismatches 112;
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                                                                                                                                                                                                                                         DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9;
                                                                                                                                                                                                                                                                                DNA (Homo sapiens)
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US-10-239-676-223
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LENGTH: 11735
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           PRIOR FILING DATE: 2001-04-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID
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DE 10019173.8
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Sequence 33, Application US/10239676 Publication No. US20030082609A1 GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
                                                                                                                                                                        APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases
FILE REFERENCE: 5013.1003
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DE 10043826.1

PRIOR FILING DATE: 2001-04-06

2000-04-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGATGTGTAGTTTTGGTTAGGATTGATGGAGGTTTCGGAGTTTTTTAAGTTTTAAT 9873
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Pred. No. 5.4;
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                                                                                                                                                                                                     Associated with Gene Regulation
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US-10-239-676-107
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US-10-239-676-107
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2000-09-01
NUMBER OF SEQ
SEQ ID NO 223
LENGTH: 6306
TYPE: DNA
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Best Local Similarity
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NUMBER OF SEQ·ID NOS:
SEQ ID NO 107
LENGTH: 6397
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                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
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                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                         TYPE: DNA
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                                       2538 GTTGGTGTTTTTTTTTTAGGTT 2561
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121 TTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGG 180
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                                                                                             TAGTTCGGGTTTGAGAAAAGGGTT 145
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o. US20030082609A1
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                                                                                                                                                           12.9%;
49.8%;
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57.6%;
                                                                                                                                                Score 46.2; DE Pred. No. 5.4; 0; Mismatches
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Pred. No. 4.9;
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SEQ ID NO 31
LENGTH: 12465
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Best Local Similarity
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                               APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, KUrt
TITLE OF INVENTION: Diagnosis of Diseases Associated with
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968 DE 10019058.8
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2000-04-06
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DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
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CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
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Pred. No. 9
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DE 10019173.8

DE 10032529.7

DE 10043826.1

PRIOR FILING DATE: 2001-04-06

2000-04-06

2000-04-07

2000-09-01

NUMBER OF SEQ ID NOS: 228

SEQ ID NO 95

LENGTH: 15732

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-239-676-95
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Search completed: June 11, 2003, 08:07:42 Job time: 52.3843 secs
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Best Local Similarity 49.8%;
Matches 143; Conservative
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                                                                                                                      194 TCTTTGGACATTTGTATTGG---ATGTTGTTGATTATTAGTGTGGACACTATTAAACCTT 250
                                                                                                                                                                                                        134 GAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTTGAG 193
                                                                                       251 AAATGGGCTTTCTATAAGGCCCCAATTATATTACGATTATAACAAAGT 297
                                                                                                                                                                                                                                                                                                                                    74 ATGATATAAAAATTTGGATAAATATTATTGGATATTCGTTTTTTAGTTCGGGTTT 133
                                                                                                                                                                                                                                                                                                                                                                             Score 45.4; DB 9; Length 15732;
Pred. No. 10;
0; Mismatches 141; Indels 3; Gaps
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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
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Perfect score:
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seq length: 2000000000
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// Cgn2_6/ptodata/1/pna/US101B_COMB.seq: *
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Copyright (c) 1993 - 2003 Compugen Ltd.
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'cgn2_6/ptodata/1/pna/US080_COMB.seq:*
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/ptodata/1/pna/US084_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US6040_COMB.seq;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Score

Query Match Length DB

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US-60-191-637-25874	US-09-614-150-25744	US-60-197-872-2063	US-09-684-016-421464	US-09-654-61/-421464	00 to the coolul	TS-10-172-096-51	US-09-865-419A-12520	US-09-619-643-14496	US-60-145-485-6295	US-09-684-016-339963	US-09-654-617-339963	US-60-255-619-17366	US-10-021-323-17366	US-09-684-016-133308	US-09-654-617-133308	US-09-803-736-1074	US-09-692-412-94	US-09-819-091A-9934	US-09-505-532-9934	US-09-502-426-1	PCT-US00-03820-1	ID
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/ptodata/1/pna/US102B_COMB

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CURRENT APPLICATION NUMBER: PCT/US00/03820
CURRENT FILING DATE: 2000-02-11
EARLIER APPLICATION NUMBER: 60/119,657
EARLIER FILING DATE: 1999-02-11
EARLIER APPLICATION NUMBER: 60/119,658
EARLIER FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 1
LENGTH: 6888
                                                                                                                                                                                                                                                                                                       Sequence 1, Application PC/TUS0003820
GENERAL INFORMATION:
APPLICANT: THE ARIZONA BOARD OF REGENTS ON BEHALF OF THE UNIVERSITY OF ARIZONA TIPLE OF INVENTION: DWF4 POLYNUCLECTIDES, POLYPEPTIDES AND USES THEREOF FILE REFERENCE: 2225-0001.40
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PCT-US00-03820-1
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Best Local (
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                                                                                                                                                                         Local Similarity
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                              TTTTTTTGCCCAATGATATAAAAATTTGGATAAATATTATTGGATATTCGTTTT
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US-60-9-528-237A-1089
US-10-221-613-29
US-60-207-458-12690
US-60-207-458-180781
US-09-656-664A-556
US-09-654-617-339755
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US-09-654-016-339872
US-09-654-016-339872
US-09-654-016-339872
US-09-654-016-339872
US-09-654-016-339872
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Pred. No. 9.2e-44;
; Mismatches 0;
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15807, A
15807, A
180781,
18013, A
339755,
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367844,
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1089, Ap
29, Appl
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61929, A
79531, A
51282, A
11950, A
11950, A
339872,
6045, Ap
28359, A
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CURRENT APPLICATION NUMBER: US/09/502,426
CURRENT FILING DATE: 2000-02-11
EARLIER APPLICATION NUMBER: 60/119,657
EARLIER FILING DATE: 1999-02-11
EARLIER APPLICATION NUMBER: 60/119,658
EARLIER FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 6888
APPLICANT: Cao, Yongwei
APPLICANT: Timberlake, William E.
APPLICANT: Timberlake, William E.
FILE REFERENCE: 38-10(15478)B
FURRENT APPLICATION UNMBER: US/09/505,532
CURRENT FILING DATE: 2000-02-16
CURRENT FILING DATE: 2000-02-16
PRIOR APPLICATION NUMBER: USSN 60/120,645 1999-02-PRIOR APPLICATION NUMBER: USSN 60/120,645 1999-02-NUMBER OF SEQ ID NOS: 51470
SEQ ID NO 9934
LENGTH: 745
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US-09-502-426-1
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US-09-505-532-9934, Application US/09505532
; GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: AZPIROZ, Ricardo
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Best Local
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APPLICANT: FELDMANN, Kenneth
TITLE OF INVENTION: DWF4 POLYNUCLEOTIDES, POLYPEPTIDES
FILE REFERENCE: 2225 0001
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USSN 60/120,645 1999-02-18; USSN 09/443,025 1999
USSN 60/120,645 1999-02-18; USSN 09/443,025 1999-11-12;
51470
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Pred. No. 9.2e-44;
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CURRENT FILING DATE: 2000-02-16
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PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: US 60/120,645
PRIOR APPLICATION NUMBER: US 60/120,645
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 09/443,025
PRIOR APPLICATION NUMBER: US 09/443,025
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 51470
SEQ ID NO 9934
LENGTH: 745
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-819-091A-9934
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US-09-819-091A-9934/c
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                                                                                                                                                                  Matches
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Best Local :
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APPLICANT: Timberlake, William E.
TITLE OF INVENTION: Plant Genome Sequences and
FILE REFERENCE: 38-10(15478)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                              Local
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                                                                               Similarity
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                                                                     TTTTTTTGCCCCAATGATATAAAAATTTGGATAAATATATTATTGGATATTCGTTTT
                                                                                                                  ATTAAACCTTAAATGGGCCTTTCTATAAGGCCCCAATTATACGATTATAACAAAGTGAC
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                                                                                                                                                                  Conservative
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99.7%;
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99.7%;
                                                                                                                                                              Score 356.4; DB 3
Pred. No. 1.6e-43;
0; Mismatches 1
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Pred. No. 1.6e-43;
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                                                                                                                                                                                      DB 31;
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US-09-692-412-94/c
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US-09-803-736-1074/c
; Sequence 1074, Application
; GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
        APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Plant Polymorphic Markers
FILE REFERENCE: 38-10(15493)D
CURRENT APPLICATION NUMBER: US/09/803,736
CURRENT FILING DATE: 2001-03-12
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APPLICANT:
                                                                                                     APPLICANT: Bush, David F.
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APPLICATION NUMBER: US 09/534,859
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                                                                             Levin, Irena M.
Norris, Susan R.
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; SEQ ID NO 94
; LENGTH: 84196
; TYPE: DIA
; ORGANISM: Arabidopsis thaliana
US-09-692-412-94
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Best Local Similarity
Matches 357; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof FILE REFERENCE: 38-10(15493)C CURRENT APPLICATION NUMBER: US/09/692,412 CURRENT FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
25792 AACTTTTACCTCGTTTTTGATCCGAAGCAATAACAAATTGTCAAATACCAAACACAAG
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                                                                                     ATTAAACCTTAAATGGGCTTTCTATAAGGCCCAATTATATATTACGATTATAACAAAGTGAC 300
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Wiegand, I
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99.7%;
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Pred. No. 1.6e-43;
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; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; OTHER INFORMATION: unsure at all n locations

US-09-654-617-133308
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US-09-654-617-133308/c
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SEQ ID NOS: 463173
SEQ ID NO 133308
LENGTH: 566
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; ORGANISM: Arabidopsis thaliana
US-09-803-736-1074
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PRIOR APPLICATION NUMBER: 1der
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 1582
SEQ ID NO 1074
                                                                                                                                                                         Matches
                                                                                                                                                                                    Query Match
Best Local
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Best Local Similarity
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                             TTAGTTCGGGTTTGAGAAAAG 141
                                                                                                              ATTAAACCTTAAATGGGCTTTCTATAAGGCCCAATTATATTATCGATTATAACAAAGTGAC 300
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 TTTNCCCAAAAAAAAAAAAAG
                                                         TTTTTTTTGCCCCAATGATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTT
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NUMBER: identified by Attorney Docket number 04983.0206CPUS01 38-10
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99.7%;
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Pred. No. 1.6e
0; Mismatches
                                                                                                                                                                       0;
                                                                                                                                                                                   Score 110.4; DB 2
Pred. No. 3.2e-07;
 93
                                                                                                                                                                       Mismatches
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APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 17366
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PRIOR FILING DATE:
20
NUMBER OF SEQ ID NOS:
SEQ ID NO 133308
LENGTH: 566
                                                                                                    US-10-021-323-17366
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; LOCATION: (1)..(566)
; OTHER INFORMATION: u
US-09-684-016-133308
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                                  Matches
                                                                   Query Match
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                                                                                                                                    ORGANISM: Gossypium hirsutum FEATURE:
                                                                                                                                                                     TYPE: DNA
                                                                                                                    OTHER INFORMATION: Clone ID: LIB3830-001-Q1-N6-B2
                                                                                                                                                                                      LENGTH: 495
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                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.8%;
Similarity 90.8%;
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                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unsure at all n locations
                                                  15.6%;
51.4%;
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Pred. No. 3.2e-07;
                                                  Score 55.8; I
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 09/654,617
                                  Mismatches
                                                                   DB 38;
                                                                                                                                                                                                                                                                                                                                      and Other Molecules Associated With
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                                                                  Lengțh
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APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Fincher, Karen E.
APPLICANT: Elegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21_(52274)A
CURRENT APPLICATION NUMBER: US/60/255,619
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 17366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LENGTH: 495
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; OTHER INFORMATION: Clone ID:
US-60-255-619-17366
                                                                                                       RESULT 11
US-09-654-617-339963/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-60-255-619-17366/c
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Best Local Simi
Matches 129;
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                                                                              Sequence 339963, Application US/09654617 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17366, Application US/60255619
TITLE OF INVENTION: Annotated Plant Genes FILE REFERENCE: 38-21(15097)D CURRENT APPLICATION NUMBER: US/09/654,617 CURRENT FILING DATE: 2000-09-05
                                                  APPLICANT: Kovalic, APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                     TTTTTTTGCCCCAATGATATAAAAAATTTGGATAAAAATATATTATTGGATATTCGTTTTT
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                                                                                                                                                                                                                                                             TAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGG
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                                                                  Kovalic, David
                                                                                                                                                                                                                                                                                                                                                                                                                              15.6%;
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Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 69;
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US-09-684-016-339963/c
; Sequence 339963/_Application US/09684016
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; ORGANISM: Zea mays
US-09-654-617-339963
  US-60-145-485-6295/c
Sequence 6295, Application US/60145485
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
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                                                     RESULT 13
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APPLICANT: Kovalic,
APPLICANT: Liu, Jingdong
TITLE OF INVENTION:
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LENGTH: 284
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SEQ ID NO 339963
LENGTH: 284
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Annotated Plant Genes FILE REFERENCE: 38-21(15097)D CURRENT APPLICATION NUMBER: US/09/684.016 CURRENT FILING DATE: 2000-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PRIOR FILING DATE:
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                                                                                                                   A 186
                                                                                                                                            TTTGCCCCAATGATATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGT 125
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Pred. No. 54;
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Pred. No. 54;
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; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3150-079-P2-N2-B2
US-09-619-643-14496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-09-619-643-14496/c
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LENGTH: 284
TYPE: DNA
TYPE: DNA
CONTROL OF THE TYPE: DNA
TYPE
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Best Local :
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Best Local 9
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APPLICANT: Miller, Philip W.

APPLICANT: MILLER, Philip W.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH TITLE OF INVENTION: PLANTS
FILLE REFERENCE: 38-21(5122)A
CURRENT APPLICATION NUMBER: US/60/145,485
CURRENT FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 9366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fisher, Dane K.
APPLICANT: Lalgudi, Raghunath V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
    158
                                                                                                   126
                                                                                                                                                                                                                                                                                                                                                                                 102;
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                                                                                                                                                                                        TITGCCCAATGATATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGT 125
Deng, Molian
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; LOCATION: (1)..(572)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3236-144-P1-N1-H3
US-09-865-419A-12520
Search completed: June 11, 2003, 05:00:52 Job time: 871.091 secs
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LENGTH: 572
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10S-10-311-455-329

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		Sequence 6. Appli		487.			279		421	1899	191		36	2148		711.	1221,	822.	90. A		187	Sequence 715. Apr

ALIGNMENTS

; TYPE: DNA ; ORGANISM: Arabidopsis thaliana US-09-502-426B-1 US-09-502-426B-1 APPLICANT: AZBITOZ, Ricardo APPLICANT: Choe, Sunghwa APPLICANT: Feldmann, Kenneth A. TITLE OF INVENTION: DW44 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF FILE REFERENCE: 11696-070001 CURRENT APPLICATION NUMBER: US/09/502,426B CURRENT APPLICATION NUMBER: US 60/119,657 PRIOR APPLICATION NUMBER: US 60/119,657 PRIOR FILING DATE: 1999-02-11 PRIOR APPLICATION NUMBER: US 60/119,658 PRIOR APPLICATION NUMBER: US 60/119,658 PRIOR FILING DATE: 1999-02-11 NUMBER OF SEQ ID NOS: 30 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 6888 Sequence 1, Application US/09502426B GENERAL INFORMATION: Query Match 100.0%; Score 358; DB 5; 100.0%; Pred. No. 7e-53;

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Best Loca Matches

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Similarity

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APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases As:
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
                                                                                                                                                                                                                                RESULT 3
US-10-311-455-1614
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; TYPE: DNA
; ORGANISM: Arabidopsis
US-09-502-426A-1
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US-09-502-426A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/502,426A CURRENT FILING DATE: 2000-02-11 PRIOR APPLICATION NUMBER: 60/119,657 PRIOR FILING DATE: 1999-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: DWF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF FILE REFERENCE: 2225-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: AZPIROZ, Ricardo APPLICANT: CHOE, Sunghwa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch 100.0%; Score 358; DB 7; Length 6888; al Similarity 100.0%; Pred. No. 7e-53; 358; Conservative 0; Mismatches 0; Indels 0
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1614
LENTH: 5449
                                                                                                                                                                                                                                                  Matches 159;
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SEQ ID NO 1196
LENGTH: 7560
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GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
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TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PRIOR DATE: 2000-09-01
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                                                                                                                                PIEPENBROCK, Christian
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Pred. No.
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         Sequence 1, Application US/10311455 GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR PPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1625
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TYPE: DNA
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                                                                                       TATATTTGATTTTTGAATGTATTTAATAA 3500
                                                                                                                                       TTAACGAAAGTTGGGTTGGTTGGAGGATTGGGTAGGTAGCGTTGGAAAGTATGTTAGTAT 3470
                                                                                                                                                                   AAACCTTAAATGGGCTTTCTATAAGGCCCAATTATATTACGATTATAACAAAGTGACAAC
                                                                                                                                                                                                  CTAGGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACTATT 243
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PIEPENBROCK, Christian
BERLIN, Kurt
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Pred. No. 0.
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CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
                                                   CURRENT APPLICATION NUMBER: US/10/240,485 CURRENT FILING DATE: 2002-10-02 PRIOR APPLICATION NUMBER: PCT/EP01/03970 PRIOR ETILING DATE: 2001-04-06 PRIOR APPLICATION NUMBER: DE 10019058.8 PRIOR FILING DATE: 2000-04-06
                                                                                                                                                                                                                                   GENERAL INFORMATION
                                                                                                                                                                                                                                            Sequence 164, Application US/10240485
       PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 PRIOR APPLICATION NUMBER: DE 10032529.7
                                                                                                                                        APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: Metastasis
FILE REFERENCE: 5013.1007
                                                                                                                                                                                          APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
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LENGTH: 7351
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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FILING DATE:
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157; Conserv
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                                                                                                                                                                                                                    US-10-312-841-2
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10312841
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
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SEQ ID NO 2
                                                                                                                                                        Matches
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Best Local Similarity
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LENGTH: 20486
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Diagnose von bedeutenden genetischen ETILE REFERENCE: E01/1208/W0 CURRENT APPLICATION NUMBER: US/10/312,841 CURRENT FILING DATE: 2002-12-30 NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                          LENGTH: 3673778
TYPE: DNA
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                                                                                                                                                                                                                               NAME/KEY: unsure
LOCATION: (379615)
                                                                                                                                                                                                                                                                            OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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                              Local Similarity
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                                                                                          TTTATGTTAAAAAATATAAATTATTTTAATTTGAAATTAAA 12174
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Pred. No. 0.26;
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TITLE OF INVENTION: Diagnosis of Diseases As:
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/PP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR PLICATION NUMBER: DE 10032529.7
PRIOR PLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 2100
TENER DEED ID NOS: 2424
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US-10-240-453-329
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Best Local Similarity 48.88;
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Sequence 329, Application US/10240453 GENERAL INFORMATION: APPLICANT: OLEK, Alexander

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                                Sequence 39, Application US/10311506
GENERAL: INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEDENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Oligoastrocytoma and Oligodendroglioma Tumor Cells
FILE REFERENCE: 5013.1015
CURRENT APPLICATION NUMBER: US/10/311,506
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/ZEP01/07539
PRIOR FILING DATE: 2001-07-02
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LENGTH: 7138
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Best Local
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TITLE OF INVENTION: Transcription
TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated
TITLE OF INVENTION: With DNA Transcription
TILE REFERENCE: 5013.1009
CURRENT APPLICATION NUMBER: US/10/240,453
CURRENT FILING DATE: 2002-10-02
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PRIOR APPLICATION NUMBER: DE 10032529.7 PRIOR FILING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TAAACCTTAAATGGGCTTTCTATAAGGCCCCAATTATATTACGATTATAACAAAGTGACAA 302
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                                                                                                                                                                                                                                                                                                                                                                                              CTTTTACTTCGTTTTTGA 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTAGGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACTAT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIEPENBROCK, Christian
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Pred. No. 0.
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0.91;
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APPLICANT: OLEK, Alexander
APPLICANT: PIEDENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Method and nucleic acids for
FILE REFERENCE: 5013.1013
CURRENT APPLICATION NUMBER: US/10/311,507
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07538
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
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US-10-311-507-39
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                                                                                                         ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-507-39
                                                                                                                                                                                NUMBER OF SEQ ID NOS:
SEQ ID NO 39
LENGTH: 14147
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LENGTH: 14147
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                                            Matches
                                                        Query Match
Best Local Similarity
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ORGANISM: Artificial Sequence
                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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                                          151;
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Similarity 48.1%;
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Pred. No. 1
                                                         Score 53.2; D
Pred. No. 1.1;
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LENGTH: 14147
                                                                                                                                                                                                                                                                                                                                                        Matches
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PRIOR TILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Method and Nucleic Acids for the Differentiation of Astrocytoma, TITLE OF INVENTION: Oligoastrocytoma and Oligodendroglioma Tumor Cells FILE REFERENCE: 5013.1015
CURRENT APPLICATION NUMBER: US/10/311,506A
CURRENT FILING DATE: 2002-12-16
CURRENT FILING DATE: 2002-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, C APPLICANT: BERLIN, Kurt
                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                                                                                                                                                                                                                                                                                                   h 14.9%;
Similarity 48.1%;
                                    CCTTAAATGGGCTTTCTATAAGGCCCAATTATATTACGATTATAACAAAGTGACAACTTT
                                                                     CGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTA 186
                                                                                                                                                                                                               GGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACTATTAAA 246
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                                                                                                                                                                                                                                                                                                                                                    Score 53.2; DB 9; Length: Pred. No. 1.1; o; Mismatches 163; Indels
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                                                                                APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases AS
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: CT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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US-10-311-455-1111
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NUMBER OF SEQ
SEQ ID NO 1111
LENGTH: 5678
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LENGTH: 384
TYPE: DNA
ORGANISM: Oryza sativa nipponbare
                                                                                                                                                                                                                                                                                                 Sequence 1111, Application US/10311455 GENERAL INFORMATION:
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Best Local 9
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                                                   PRIOR APPLICATION NUMBER: DE 10043826.1 PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                               APPLICANT: OLEK, Alexander
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APPLICANT: Bougri, Olegs
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51892)B
FULR REFERENCE: 38-21(51892)B
CURRENT APPLICATION NUMBER: US/09/837,604A
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 60/197,872
PRIOR FILING DATE: 2000-04-19
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NAME/KEY: unsure
LOCATION: (1)..(384)
OTHER INFORMATION: unsure at all n locations
FEATURE:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Clone ID: LIB3431-010-P1-K1-A7
                                                                                                                                                                                                                                                                                                                                                                                                        151 TTATATATTTTT
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Shukla, Hridayabhiranjan
                                    IJ
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Listing first 45 summaries
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Perfect score:
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                                  137.4
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                                                                                                        Score
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358
1 aaaaaaaaaaagatgaaagt.....tgtcaaataccaaacacaag 358
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Copyright (c) 1993 - 2003 Compugen Ltd.
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gb_est2:*
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AL071865 Drosophii
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52.2	52.2	52.2	52.4	52.4	52.4	52.6	52.8	<u>υ</u>	53	53.2	53.2	53.4	53.4	53.6	53.6	53.6	54	54	54	54.2	54.2	54.4	54.6	54.6	54.6	54.8	55	55.6	51	56	25.0	56.4	56.6	56.6	57	57.8	58	58.2
14.6	14.6	14.6			14.6	14.7	14.7	٠	14.8	14.9		•	•	15.0	•	15.0	15.1	15.1	15.1	15.1	15.1	15.2	15.3	15.3	15.3	15.3	•		л :			15.8	٠	5	15.9	6	16.2	16.3
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ALIGNMENTS

REFERENCE 3 REFURENCE 3 RAUTHORS LI TITLE DI JOURNAL SU		JOURNAL UI REFERENCE 2	TITLE A	REFERENCE 1 AUTHORS SI	R SI	SOURCE tl		ACCESSION A	DEFINITION A	543
Unpublished (bases 1 to 176) Li,Y., Strizhov,N., Rosso,M. and Weisshaar,B. Direct Submission Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer	ROSSO,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics	transformed lines Unpublished	and Weisshaar,B. A pipeline for automated high-throughput generation of FSTs (flanking segmence tags) from arabidonsis thalians T.DNA	<pre>1 Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.</pre>	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	thale cress. Arabidopsis thaliana	AL762543.1 GI:21508636 GSS	genomic survey sequence. AL762543	AL/62543 176 bp DNA linear GSS 19-JUN-2002 Arabidopsis thaliana T-DNA flanking sequence GK-025G03-013722,	

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      Submitted (17-JUN-2002) Weisshaar
                       3 (bases 1 to 194)
L1,Y., Strizhov,N., Rosso,M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic survey sequence.
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                                                                                    Unpublished
                                                                                                       for flanking sequence
                                                                                                                                                   Rosso, M.,
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                                                                                                                       M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence processed for submission. T-DNA derived sequences were removed. 27 g 56 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC106. The lines contain one or more T-DNA
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http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was
as reported previously (Seki et al., 1998).
                                                                           3-1-1 Koyadai, Tsukuba,
Tel: 81-298-36-4359
Fax: 81-298-36-9060
                                                                                                                                                                     Contact: Motoaki Seki
Plant Functional Genomics Research Group
                                                                                                                                                                                                                   Large scale analysis of Arabidopsis full-length cDNA (2002b) Unpublished (2002)
                                                                                                                                                                                                                                                                    Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                Seki.M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Aggnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 423)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib "Arabidopsis thaliana T-DNA insertion lines"
/note "PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC106. The lines contain one or more T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:3702"
/clone="GK-025G03-013757"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:19806408
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Pred. No. 2.1
                                                                                                                            Ibaraki 305-0074,
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         constructed essentially This clone is in a
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)6-76-F19 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1:
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Gaps

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RESULT 4
CNS00LT2
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                          source
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                                                                                                                          Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Marton Mammoser in Pletter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-88 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL078714.1 GI:5102004 GSS.
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BACR48P19 of RPCI-98 library from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified pBluescript vector as a SstI/XhoI insert. Please visit our
web_site_(http://www.gsc.riken.go.jp/e/plant/index _e.html) for
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
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                                                                                      and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic survey sequence.
                                                              at http://bacpac.med.buffalo.edu/drosophila_bac.htm
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germination to mature seeds"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Site_1: SstI; Site_2: xhoI; subjected
dehydration (1, 2, 5, 10, 24 hr) and cold (1,
hr) treatments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis
/db_xref="taxon:3702"
/clone="RAFL06-76-F19"
/clone_lib="RAFL6"
                                        Location/Qualifiers
/organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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                                                                                                                                                Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNS00DKY 928 bp DNA linear GSS 04 Drosophila melanogaster genome survey sequence T7 end of F BACR27A24 of RPCI-98 library from Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 928)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
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                                                                                                                                    found at http://bacpac.med.buffalo.edu/drosophila_bac.htm
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/clone="BACR48919"
/clone_lib="RPCI-98"
/note="end: TET3"
a 6 c 69 g
                                        /organism="Drosophila melanogaster
/db_xref="taxon:7227"
                                                                                                         Location/Qualifiers
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                           ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                        The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Manunoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
                                                                                                                                                                                                                                                                                                                                     - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a Collaboration with the Berkeley Drosophila Genome Project (BDGP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster genome survey sequence T7 end of EBACR17N06 of RPCI-98 library from Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNS00KHX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomic survey sequence.
   /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR17N06"
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31.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                     Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a language clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS;
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                                                                                                                                                                                                                                                               2 (bases 1 to 1027)
Roest-Crollius, H., Jaille
Bouneau, L., Billault, A.,
                                                                                                                                                                                                                                                                                                                                                                          Roest-Crollius,H., Jaillon,O., Das
Bernot,A., Fizames,C., Wincker,P.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontidae; Tetraodon.

1 (bases 1 to 1027)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNS02T50 1027 bp DNA linear GSS 15-MAY.
Tetraodon nigroviridis genome survey sequence T7 end of clone
163M16 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                  Direct Submission
                                                                                                                                                      Genoscope.
                                                                                                                                                                                                                                                                                                                                                            Human gene number estimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tetraodon nigroviridis
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                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                 Weissenbach,J.
                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                         Tetraodon nigroviridis
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/note="end : T7"
a 82 c 77 g
Location/Qualifiers
1. .1027
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                                                                                                                                                                                                                                                             Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Lt,A., Quetier,F., Saurin,W., Bernot,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59;
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                                                                                                                                                                                                                                                                                                                                   mate provided
DNA sequence
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Reoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                            - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genome survey sequence T7 end or \tt BACN16D22 of DrosBAC library from Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                  project grant.
and Genevieve
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/note="end : T7"
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/note="Genoscope sequence ID : COAG163BG08LP1-end : 86 c 100 g 381 t 130 others
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/db_xref="taxon:7227"
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/db_xref="taxon:99883"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence start: High quality sequence stop: 2
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/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR); Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
                                                                                        whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and Barell, Oxford University Press, 1999)."
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/db_xref="taxon:5759"
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  16.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
       121 TTAGTTCGGGTTT-----
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                        /clone="BACR29K22"
/clone_lib="RPCI-98"
/note="end : T7"
a 140 c 25 g
                                                                                                                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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42.1%;
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     -GAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATAT 173
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                                                                                                                                                                         08
                                                                                                                                                                                                                                                 Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 894)
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                                                            ACCTWAYCCWKTTGCCAAKKTGKTWTWTTTTTTTTTKTTKKTTWTTTKKTTTAGGGKTTAT 105
                                                                                                                                      TTWTKATWWAKTKAYGTWTTTTKKTTWKTWTWWTTATTTKWCTKWTTTWTKTWTGWTWTK 165
                                                                                                                                                                         TATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTTCGGGTTTGAGAAA 139
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/note="end : T7"
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/clone_lib="DrosBAC"
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/db_xref="taxon:7227"
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AL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, Cp 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrefégenoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen exiguus, Saccharomyces bayanus var. uvarum, Saccharomyces servazzii, Zygosaccharomyces rouxii, lactis var. lactis, Kluyverinyces thermotolerans, Kluyveromyces angusta, Debaryomyces hansenii var. hansenii, Pichia candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to keywords for description of this sequence and for the sequence of the other extremity of this insert.
     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R., Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M. Genomic exploration of the hemiascomycetous yeasts: 11.

REBS Lett. 487 713
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Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potter, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Mesolowski-Louvel, M.,
Wincker, P., and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
FIBS Lett. 487 (1), 3-12 (2000)
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Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
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/clone="BA0AB018F06"
                                                                                                                                                                                                                      /variety="lactis"
                                                                                                                                                                                                                                               /organism="Kluyveromyces lactis"
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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/plasmid="pBeloBAC11"
/note="end: T7"
288 c 267 g
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/db_xref="taxon:7227"
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AUTHORS

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GSS 26-JUL-1999

ACCESSION VERSION

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Submitted (02-JUN-1999) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (E-mail :
- Web : www.genoscope.cns.fr)
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                          TATTAAACCTTAAATGGGCTTTCTATAAGGCCCCAATTATATTACGATTATAACAAAGTGA 299
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/note="end : TET3"
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/db_xref="taxon:7227"
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segref@genoscope.cns.fr
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Search completed: June 11, Job time : 545.722 secs
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                                                                                                                                                                                                                                                                                                                        74;
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fi Bouneau, L., Billault, A., Quetler, F., Saurin, W., Bernot, A. Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetler, F., Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using Tetracdon nigroviridis DNA sequence
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Tetraodon nigroviridis.
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/note="Genoscope sequence ID : C0BG095CC10LP1~end
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/db_xref="taxon:99883"
/clone="095F19"
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                      2003,
                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                          Score 56; |
Pred. No. 7
                                                                                                                                                                                                                                                                                                                          Mismatches
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survey sequence T7 end of clone
aodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                           DB 17; Length 949
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nigroviridis
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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                    2681
978.5
978.5
978.5
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Gapop 10.0 , Gapext 0.5
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1553.581 Million cell updates/sec
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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AAW27153
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               A cytochrome P450
Arabidopsis thalia
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  Taxus
cuspidata
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45	44	43	42	41	40	39	38	37	36	. σ	34	ω ω	32	<u>ω</u>	30	2.9	28	27	26) K.	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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497	433	492	492	492	492	388	503	481	489	498	512	483	500	484	500	493	501	484	507	509	496	497	485	430	469	479	471	468	465	462	461	465	462	461
19	21	23	22	19	19	21	22	21	21	22	22	22	22	22	22	22	22	22	22	22	22	22	22	21	21	21	21	21	21	21	21	21	21	21
AAW37735	0	32	AAB85155	AAW44159	AAW37733	AAG20785	AAU02828	AAG30049	AAG30048	AAU02838	AAU02834	AAU02827	AAU02826	AAU02821	AAU02824	AAU02836	AAU02823	AAU02822	AAU02830	AAU02832	AAU02837	AAU02829	AAU02835	AAG20784	AAG23014	AAG23012	_	AAG20783	AAG11834	AAG11835	AAG11836	AAG46491	AAG46489	AAG46490
Cytochrome P450RAI		Zebrafish P450RAT	Zebrafish cytochro	Zebrafish retinoid	Cytochrome zP450RA	Arabidopsis thalia	י.כ		dopsis thal	cuspidata		cuspidata	cuspidata		cuspidata	2		0 6	Arabidone's thalia	0 0		thali	thali	thali	+ ha 1	is thali	Arabidopsis thalia							

ALIGNMENTS

RESULT 1

PT New isolated dwf4 polynucleotide useful for altering the phenotype of PT plants, for diagnostic assays and in the production of antibodies -	DR WPI; 2000-549142/50. DR N-PSDB; AAA59599.	PI Azpiroz R, Choe S, Feldmann KA;	PA (ARIZ-) ARIZONA BOARD OF REGENTS.	PR 11-FEB-1999; 99US-0119657. PR 11-FEB-1999; 99US-0119658.	PF 11-FEB-2000; 2000WO-US03820.	PD 17-AUG-2000.	PN WO200047715-A2.	OS Arabidopsis sp.	KW DWF4; cytochrome P450 enzyme; bra KW plant phenotype; cell elongation. XX	DE A cytochrome P450 enzyme designated DWF4.	AC AAB07921;	ID AAB07921 standard; Protein; 513 AA.	AAB07921
e useful for altering the ph		А;	Š.						P450 enzyme; brassinosteroid; 22alpha-hydroxylation; cell elongation.	nated DWF4.		3 AA.	
enotype of bodies -									roxylation;				

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RESULT 2
AAW27153
ID AAWY
XX AW
AC AAW
XX
AC AAW
XX
XX
DE Aral
XX
Cytc
KW Cytc
KW Cytc
KW bras
KW teas
XX
XX
XX
XX
XX
Aral
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                                                             Cytochrome P450-type hydroxylase; identification; brassinosteroid, brassinosteroid inhibitor; modified plant; recombinant production;
                  Arabidopsis
                                                                                                                    Arabidopsis
                                                                                                                                                   14-APR-1998
                                                                                                                                                                                                                   AAW27153 standard; Protein; 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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                                                                                                                                                                                                                                                                                                  GKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEA
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                                                                                                                                                                                                                                                                                                                                                                                                    QPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFTHHLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                      YKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILK
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                                                                                                                                                                                                                                                                                                                                                                                                                                     YKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQ
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                                                                                                                                                  (first
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                                                                                                                                                  entry)
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                                                                                                                 cytochrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2681; DB 21;
Pred. No. 1.3e-228;
                                                                                                                 P450-type
                                                                                                                                                                                                                     ₽
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                                                                                                                 hydroxylase
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plants with modified physiological and/or phenotypic characteristics. The modified plants may show, e.g. stimulation growth, increased cell elongation, increased wood production, accelerated seed germination at low temperatures, an increase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dry weight, repressed anthocyanin production during growth in light and/or inhibited de-etiolation which is induced, e.g. by cytokinin, in the dark or an increase in stress tolerance. The hydroxylase or its coding sequence can also be used for the recombinant production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Pages 44-46; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated plant cytochrome P450-type hydroxylase gene - used to identify substances acting as brassino-steroid(s) or brassinosteroid inhibitors for the production of modified plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P450 type hydroxylase. The hydroxylase can be used to identification brassinosteroids or brassinosteroid inhibitors, useful to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Altmann T,
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491
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                                                                                                                                                                 GYETTSTIMTLAVKFLTETPLALAQLKEEHEKIRAMKSD--SYSLEWSDYKSMPFTQCVV
                                                                                                                                                                                                                                                                                                                     IMSMDPGEEETEQLKKEYVTEMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEERKL
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DQPFAFPFVDFPNGLPIRVSR
                                                   QQNNGASSSGSGSTSTWGNN-YMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAED
                                                                                                                                 NETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQ
                                                                                                                                                                                                                                    VVVMKRREEEEEGAE
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                                                                                                                                                                                                                                                                                                                                                                                                    MHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLLLSSIAAGFL----LLLRRTRYRRMGLPPGSLGLPLIGETFQLIGAYKTENPEPFIDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLLLPSLLSLLLFLILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQH
                                                                                                  NETLRVANIIGGVFRRAMTDVEIKGYKIPKGWKVFSSFRAVHLDPNHFKDARTFNPWRWQ
                                                                                                                                                                                                                                                                                                    LMSFDPG-EWSESLRKEYLLVIEGFFSLPLPLFSTTYRKAIQAR-----RKVAEALT
                                                                                                                                                                                                                                                                                                                                                                                                                                     VARYGSVFMTHLFGEPTIFSADPETNRFVLQNEGKLFECSYPASICNLLGKHSLLLMKGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       472 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Pred. No. 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ); DB 18;
5.6e-78;
hes 171;
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99US-0139463.
99US-0139463.
99US-0139763.
99US-0140055.
99US-014005.
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Query Match
Best Local Similarity
Matches 210; Conserv
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990S-0160989
990S-0161404
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99US-0158039
99US-0159293
                                                                                                                                                                               36.5%; Score 978.5; DB 21;
41.9%; Pred. No. 6.6e-78;
tive 79; Mismatches 171;
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ID AAG44
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/9; Mismatches 171;
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                                                                            EP1033405-A2
                                                                                                       Arabidopsis thaliana
                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200210210-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herbicidally active polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB91571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB91571 standard;
                                                                                                                                                                                                                                                                                                                         Local
                    282
                                               250
                                                                       222
                                                                                                191
                                                                                                                                                     131
                                                                                                                           162
                                                                                                                                                               102 QNEGRLFECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHT
                                                                                                                                                                                                                                                                                                             181;
                                                                                                                                                                                                        71
                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                    11 LLSVSSSTTFLAFIIIFLLAGIARRKRRAPHRLPPGSRGWPLIGDTFAWLNAVAGSHPSS
                                                                                                                                                                                                                                                                            12 LLLLPSLLSLLLFLIL-----LKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGD
                                                                                                                                                                                                                                                                                                                         Similarity
DLPGFTYNKAMKARKEIIRKINKTIEKRLQNKAASD-
                                                                NLPGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQR
                                                                                         LQTLSNFKDGEVVLLQDICRKVAIHLMVNQLLGVS-SESEVDEMSQLFSDFVDGCLSVPI
                                                                                                                    LFVLDSWQQNSIFSAQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPL
                                                                                                                                              QNEGKLFQSSYPKSFRDLVGKDGVITVHGDQQRRLHSIASSMMRHDQLKTHFLEVIPVVM 190
                                                                                                                                                                                                FVEKQIKKFVSLLCSVLLLILKRPDNSGFNEIRYGRIFSCSLFGKWAVVSADPDFNRFIM 130
                                                                                                                                                                                                                                 FMQQHVSK-
                                                                                                                                                                                                                                                                                                                                                                512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weidler
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plant; agriculture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                    32.3%; Score 866; 33.8%; Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26lpp + Sequence Listing;
                                                                                                                                                                                                                                                                                                            105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    512
                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO
                                                                                                                                                                                                                           ----YGKIYRSNLFGEPTIVSADAGLNRFIL
                                                                                                                                                                                                                                                                                                                     DB 23;
5.8e-68;
                                                                                                                                                                                                                                                                                                                                  Length 512;
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                       76;
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plant
                                                                                                                                                                                                                                                                                                                                                                                                               them
                                                                                                                                                                                                                                                                                                                                                                                                                                                  using
               341
                                                                                           249
                                                                                                                                                                                                                           101
                                                                                                                     221
                                                                                                                                                                        161
                                                                                                                                                                                                                                                                             66
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밁 Q

20

LFICVILLLERSNDRQGNGSANKPKLPPGSAGLPFIGETIRFLRDAKSPGRRKFFDEHE 79 LSLLLFLILLKRRNRK-----TRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQHV 72

19

Query Match Best Local S Matches 176

Similarity

30.5%;

Conservative

97;

Score 816.5; DB: Pred. No. 1.5e-63 7; Mismatches 18

184; 22;

Indels Length

Gaps

8

100

486; 45;

سليانا أغلمانيا أم

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RESULT 10
AAUU2839
ID AAUU2839
XX AAUU2839
AC AAUU2
XX AAUU2
XX AAUU2
XX O7-SE
XX O7-SE
XX OXYG
KW CXYG
KW CXYG
KW CXYG
KW CXYG
KW Tran
XX Taxu
PN W02(
XX 13-
XX C
PF 13-
XX 
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                                            The sequence represents a Taxus cuspidata oxygenase, encoded by a DNA of the invention. The sequences isolated from the Taxus genus, and the respective oxygenases are useful for the synthetic production of Taxol and related taxoids, as well as intermediates within the Taxol blosynthetic pathway, and other taxoid derivatives. The sequences also can be used to make transgenic organisms that either produce the oxygenases for subsequent in vitro use, or produce the oxygenases in vivo so as to alter the level of Taxol and taxoid production within the useful for isolating the polynucleotide and polypeptide sequences useful for isolating the polynucleotide and polypeptide sequences
   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 139-141; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acid and amino acid sequences, isolated from genus, useful for the synthetic production of Taxol and retaxoids, intermediates within the Taxol biosynthetic pathw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAS05196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Croteau RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxygenase; Japanese yew; transgenic organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UNIW ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200134780-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Taxus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Taxus cuspidata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU02839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU02839 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-355489/37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287 AGNGVLGRLLEEESLPNESMADFIINLLFAGNETTSKTMLFAVYFLTHCPKAMTQLLEEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cuspidata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  taxoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTRFCPGAELARLQIALFLHYFITTYKWTQLKEDRISFFPSARLVNGFKIQLNR 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPNGLPIRVSR 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCFVVPFLSAVHLDESYYKESLSFNPWRWLDPETQQKRNWRTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GWKVLPVISAVHLDNSRYDQPNLFNPWRW-----QQQNNGASSSGSGSFSTWGNNYMPFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LETARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----DRLAGGMLTWQDYKTMDFTQCVIDETLRLGGIAIWLMREAKEDVSYQDYVIPK
486 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WASHINGTON STATE RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schoendorf A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0165250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Taxol; taxoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jennewein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pathway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the Taxus
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RESULT 11
AAG46490
ID AAG46
XX
AC AAG46
XX
DT 18-OX
XX
Prot
XW hybr
XW tern
XX
FN EP1
XX
PR 25-
PR 05
PR 05
PR 25-
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    25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
25-MAR-1999
01-APR-1999
01-APR-1999
16-APR-1999
16-APR-1999
21-APR-1999
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23-APR-1999
30-APR-1999
30-APR-1999
                                                                                                                                                                                                                                                                                                            06-SEP-2000
                                                                                                                                                                                                                                                                                                                                          EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis
                                                                                                                                                                                                                                                                               25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG46490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG46490 standard; Protein; 461 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQDNLFNDWRWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RATYFPLPSTENGFPIRLYSRV 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NETLRLGGATVVLFREAKQDIKVKDFVIPKGWTVSVFLSATHVDGKYHYEADKFLPWRWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           thaliana protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                               2000EP-0301439
    990S-0123548

990S-0125788

990S-0126785

990S-0126785

990S-0127462

990S-0128714

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990S-013049

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                                                                                                                                                                                                                                                                                                                                                                                                               promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                          pathway;
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05-MAY-1999;
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Matches 166
           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                 AAG46489 standard; Protein; 462
                                                   Arabidopsis
                                                                                              AAG46489;
          termination sequence
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HYFVTRYRWEEIGGDELMVFPRVFAPKGFHLRIS 459
                                                                                                                                                                                           HHLVLKFNWELAEDDQPFAFPFVDFPNGLPIRVS 510
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                                                                                                                                                                                                                             SRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPEGGGPRICAGSELAKLEMAVFI 476
                                                                                                                                                                                                                                                          GLEDVKSMKFTRAVIYETSKLATIVNGVLRKTTRDLEINGYLIPKGWRIYVYTREINYDA
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                                             thaliana protein fragment SEQ ID NO: 58493,
                                                                       (first entry)
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99US-0160814
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99US-0160981
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99US-0161405
99US-0161406
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99US-0161351
99US-0161392
99US-0161992
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99US-0161992
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32.3%;
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Pred. No. 1.5e-55;
1); Mismatches 181;
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23-AUG-1999; 25-AUG-1999; 26-AUG-1999;

99US-

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99US-0150884. 99US-0151065. 99US-0151066. 99US-0151080. 99US-0151303.

99US-0151303 99US-0151438

11-AUG-1999 12-AUG-1999 13-AUG-1999 13-AUG-1999 16-AUG-1999 17-AUG-1999 18-AUG-1999

990S-0147302 990S-0147360 990S-0147360 990S-0147363 990S-0147416 990S-0147935 990S-014821 990S-0148341 990S-0148341 990S-0148341 990S-0149368 990S-0149368 990S-01494725 990S-0149722 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0149723

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28-SEP-1999; 29-SEP-1999; 04-OCT-1999; 05-OCT-1999; 06-OCT-1999; 07-OCT-1999;

14-OCT-1999 14-OCT-1999

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16-SEP-1999

99US-0153758. 99US-0154018. 99US-0154039. 99US-0154779. 99US-0155139. 99US-0155486.

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29-SEP-1999;
04-OCT-1999;
05-OCT-1999;
06-OCT-1999;
07-OCT-1999;
08-OCT-1999;
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16-SEP-1999;
20-SEP-1999;
22-SEP-1999;
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                                                                                                                                                                                                                                                                                                   70 QHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLV 129 :| | :| : | | | :| : | : | :| :
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    NWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDN 416
                                                                                                                                                                                                                       GSSHRLMRGSLLSLISSTMMRDHILPKVDHFMRSYLDQWNELEVIDIQDKTKHMAFLSSL
                                            FIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSN----L
                                                                                                                                                              TQIAGNLRKPFV------EEFKTAFFKLVVGTLSVPIDLPGTNYRCGIQARNNIDR
                                                                                                                                                                              ----NLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILK
                                                                                                              LLRELMQERR----
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99US-0159294.
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99US-0159329.
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990S-0161405

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990S-0161920

990S-0161923

990S-0161993

990S-0161993
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990S-0159331.
990S-0159637.
990S-0159638.
990S-0159584.
990S-0160761.
990S-0160767.
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99US-0158232.
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; Pred. No. 1.5e-55;
91; Mismatches 181;
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                                                                                                        TFTDMLGYLMKKEGNRYPL
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   RESULT 13
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24-MAY-1999
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01-JUN-1999
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08-JUN-1999
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23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
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30-APR-
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23-APR-
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05-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318 GLEDVKSMKFTRAVIYETSRLATIVNGVLRKTTRDLEINGYLIPKGWRIYVYTREINYDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000EP-0301439
99US-0134218

99US-0134219

99US-0134370

99US-0134761

99US-0134941

99US-0135124

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                                                                       LLQIAETLKKPEVEEYRTEFFKLVVGTLSVPIDIPGTNYRSGVQARNNIDRLLTELMQER
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93; Mismatches 196;
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Db	Qy	DЪ	ρ	DЪ	Qy
436 EENGEDKLMVFPRVSAPKGYHLKCS 460	486 ELAEDDQPFAFPFVDFPNGLPIRVS 510	387 NPWRWMEKSLESKSYFLLFGGGVRLCPGKELGISEVSSFLHYEVTKYRW 435	GSGSFSTWGN	327 FTRAVIFETSRLATIVNGVLRKTTHDLELNGYLIPKGWRIYVYTREINYDTSLYEDPMIF 386	366 FTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLF 425

Search completed: June 10, 2003, 21:57:23 Job time: 46 secs

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241.5 9.0 502 4 US-09-499-302A-4 241.5 9.0 531 4 US-09-380-420C-2 241 9.0 490 4 US-09-126-420A-16 241 9.0 510 4 US-09-66-505B-66 240.5 9.0 510 4 US-08-616-990-66 240.5 9.0 509 3 US-08-948-564-18 239 8.9 496 1 US-08-313-075A-50 236 8.7 490 1 US-08-201-118-1 234.5 8.7 490 1 US-08-201-118-1 234.5 8.7 490 5 PCT-US95-05744-1 233.5 8.7 490 5 PCT-US95-05744-1 233.5 8.7 508 4 US-08-91-677-2 232.5 8.7 508 4 US-08-91-677-2 232.6 8.6 506 1 US-08-313-075A-38 231 8.6 506 3 US-08-606-505B-65 225.5 8.4 471 4 US-09-126-420A-20
5302 5302 5302 5303 5304
444W4WHWHWA44
4 US-09-499-302A-4 4 US-09-380-420C-2 4 US-09-126-420A-16 3 US-08-616-990-66 4 US-09-616-990-66 3 US-08-948-564-18 1 US-08-948-564-14 1 US-08-948-564-1 1 US-08-91-677-2 1 US-08-91-677-2 1 US-08-91-677-2 2 US-08-91-675A-38 3 US-08-666-595B-65 4 US-09-302-620B-95 4 US-09-302-620B-95
US-09-380-420C-2 US-09-380-420C-2 US-09-126-420A-16 US-08-666-5058-66 US-08-666-5058-50 US-08-948-564-14 US-08-948-564-14 US-08-948-564-14 US-08-948-564-14 US-08-91-677-2 US-08-91-677-2 US-08-91-677-2 US-08-91-678-38 US-08-666-5058-65 US-09-616-990-65 US-09-616-990-65 US-09-126-420A-20

ALIGNMENTS

KONCZ, CSABA MATHUR, JAIDEEP

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US-08-622-166A-2
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/622,166A
                                                                                                                                                                                                                                                                                             APPLICATION UMBER: US/08/622,
FILING DATE: 27-MAR-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SVENSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 0147
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                      TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INTERPOLEMENTS: 4
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
CORRESPONDENCE Birch, Stewart,
                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SZEKERES, MIKLOS
APPLICANT: ALTMANN, THOMAS
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING CYTOCHROME
TITLE OF INVENTION: P450-TYPE PROTEINS INVOLVED IN THE BRASSINOSTEROID SYNTHESI
                                                                                                                                                                                  TYPE: amino acid TOPOLOGY: linear
                                                                 Local Similarity es 210; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Birch, St. STREET: P.O. Box 747 CITY: Falls Church STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 22040-0747
12 LLLLPSLLSLLLELILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFWQQH 71.
                                                               Conservative
                                                      36.5%; Su.
/ 41.9%; Pre/
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                                                                                                                                                                                                                                                                                                                                                                 0147-0153P
                                                                                  Score 978.5; DB Pred. No. 5e-89;
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                                                          Mismatches 171;
                                                                                                  DB 2;
                                                            Indels 41;
                                                                                                  Length 472;
                                                          Gaps
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US-08-622-166A-4
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Patent No. 595254
   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: KONCZ, CSABA
                                                  REFERENCE/DOCKET NUMBER: 30,330
TELECOMMUNICATION INFORMATION:
TELEPHONE: (733) 205-8000
TELEPAX: 777.3
                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 27-MAR-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MATHUR, JAIDEEP
APPLICANT: SZEKERES, MIKLOS
APPLICANT: ALTMAN, THOMAS
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING CYTOCHROME
TITLE OF INVENTION: P450-TYPE PROTEINS INVOLVED IN THE BRASSINOSTEROID SYNTHESIS
NUMBER OF SEQUENCES: 4
                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                             TELEFAX: (703)
TELEX: 248345
                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Birch, St
STREET: P.O. Box 747
CITY: Falls Church
                                                                                                                                                                                                                                     SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08622166A
                                                                                                                                                                                                                                                                                                                                                     Virginia
                                                (703) 205-8050
                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                  Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                  Stewart,
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                                                                                                    0147-0153P
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US-08-724-466B-2
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Best Local Sim.
Matches 210;
                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08724466B Patent No. 6063606
                                                                                                                                                                                                                                                                                                                                                       GENERAL
                             APPLICATION NUMBER: US/08/724,466B FILING DATE: October 1, 1996 PRIOR APPLICATION DATA:
                                                                             SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch,
                                                                                                                                                                                                                                                                                    APPLICANT: Petkovich, P. Mar
APPLICANT: Beckett, Barbara
TITLE OF INVENTION: Retinoid
NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 472 amino
                                                                                                            COMPUTER: COMPAQ, IBM PC
OPERATING SYSTEM: MS-DOS
APPLICATION NUMBER: 0 FILING DATE: June 21,
                                                                                                                                                                                   ZIP: M5L 1A9
COUNTRY: Canada
                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 VVVMKRREEEEEGAE-------RKKDMLAALLAADDGFSDEEIVDFLVALLVA
                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 LLLLPSLLSLLLFLILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQH 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
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                                                                                                                                                                                                                    Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVI 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLLLSSIAAGFL----LLLRRTRYRRMGLPPGSLGLPLIGETFQLIGAYKTENPEPFIDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKLVFFPTTRTQKRYPIFVKR 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DQPFAFPFVDFPNGLPIRVSR 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQNNGASSSGSGSFSTWGNN-YMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMSFDPG-EWSESLRKEYLLVIEGFFSLPLPLFSTTYRKAIQAR-----RKVAEALT
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                                                                                                                                                                                                                                   Box 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                     Blake,
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                                                                                                                                                                                                                                   Commerce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -SNSVTTGPSNVFTPFGGGPRLCPGYELARVALSVFLHRLVTGFSWVPAEQ
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ommerce Court West
   08/667,546
1, 1996
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                                                                                                                 compatible 5.1
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                                                                                                                                                  1.4 Mb storage
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                                                                                                                                                                                                                            Sequence 2, Application US/08882164D Patent No. 6306624 GENERAL INFORMATION:
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TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 2:
                                STREET: bc..
CITY: Toronto
TMATE: Ontario
Canada
                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon STREET: Box 25, Commerce Court West
                                                                                                                                          APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein NUMBER OF SEQUENCES: 43
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
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              COUNTRY: Canada
ZIP: M5L 1A9
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STRANDEDNESS: sin
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 467 LAKLEMAVFIHHLVLKFNWELAEDDQ-----PFAFPFVDFP 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 5076
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (416) 863-2653 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: June 25, 1997
PRIOR APPLICATION DATA:
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TYPE: amino acid
STRANDEDNESS: sir
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COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
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                                                                                                                                                                                                                    351 LG----ESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKYL
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443 FAKVLLKIFLVELTQHCNWILSNGPPTMKTGPTIYPVDNLP 483
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                                          LAKLEMAVFIHHLVLKFNWELAEDDQ-----PFAFPFVDFP 502
                                                                                     YSICDTHDVADVFPNKEEFQPERFM-----SKGLEDGSRF--NYIPFGGGSRMCVGKE
                                                                                                                                PVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSE
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RESULT 5
US-08-882-164D-32
US-08-882-164D-32
; Sequence 32, Application US/08882164D
; Patent No. 6306624
; Patent No. 6306624
; GENERAL INFORMATION:

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INFORMATION FOR SEQ ID NO: 32
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local 9
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FILING DATE: June 21,196
APPLICATION NUMBER: 08/724,466
FILING DATE: OCLOBET 1,1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REPERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskette, 3 1/2 inch, 1
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:

ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/882,164D FILING DATE: June 25, 1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 17.2%; Score 461; DB 4; Length 497; Local Similarity 28.4%; Pred. No. 2.4e-37; Less 148; Conservative 78; Mismatches 231; Indels
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CITY: Toronto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 GILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQ--NSIFS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
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PVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSE 466
                                                             LCKSNODNKLDMETLEOLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYOIPKGWNVI 395
                                                                                                   AKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVL 406
                                                                                                                                               ---ALKQS--STE-----LLFGGHETTASAATSLITYLGLYPHVLQKVREEIKSKGL
                                                                                                                                                                                                                                   VKARNLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWE-----RGERLDMQ- 288
                                                                                                                                                                                                                                                                                                                       VYPEVKRLMFRIAMRILLGCEPGPAGGGEDEQQLVEAFEEMTRNLFSLPIDVPFSGLYRG
                                                                                                                                                                                                                                                                                                                                                                 AQDEAKKFTFNLMAKHIMSMDPGE----EETEQLKKEYVTFMKGVVSAPLNLPGTAYHKA 231
                                                                                                                                                                                                                                                                                                                                                                                                         TILGAGCLSNLHDSSHKQRKKVIMQAFSREALQCYVLV-IAEEVSSCLEQWLSCGERGLL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPALLASALCTFVLPLLLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETL---- 58
                                                                                                                                                                                     LGWYLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIAR
                                                                                                                                                                                                                                                                           LQSRATILKFIERKMEE---RKLDIKEED----QEEEEVKTEDEAEMSKSDHVRKQRTDDDL 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -OMVLORRKFLOMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVHWPASVR 117
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                                                                                                                                                 335
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283 DDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHL 342	Qγ	
233 LYRGMKARNLIHARIEQNIRAKICGLRASEAGQGCKDALQLLIEHSWERGERL 285	Db	
228 YHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRT 282	Qy	
GCEPQLAGDGDSE-QQLVEAFEEMTRNLFSLPID	рь	
173 IFSAQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFNKGVVSAPLNLPGTA 227	Qу	
:: :: : : :	Db	
118 GILGKWSMLVLVGDMHRDMRSISLNELSHARLRTILLKDVERHTLFVLDSWQQNS 172	Qy	
59 -QMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWPASVR 117	Db	
58 PYTATTLGDEMQQHVSKYGKIYRSNLEGEPTIVSADAGLNREILQNEGRLFECSYPRSIG 117	Qy	
3 LPALLASALCTFVLPLLLFLAAIKLWDLYCVSGRDRSCALPLPPGTMGFPFFGETL 58	Db	
10 LPLLLLPSLLSLLLFLILLKRRNRKTRFNLPPGKSGWPFLGETIGYLK 57	Qy	
y Match 16.4%; Score 439; DB 3; Length 497; Local Similarity 27.0%; Pred. No. 3.7e-35; hes 142; Conservative 85; Mismatches 226; Indels 72; Gaps 15;	Query M Best Lo Matches	
TOPOLOGY: linear 724-466B-4	US-08-	
S	•• ••	
FOR SEQ	; INF	
TELEPHONE: (416) 863-4344 TELEPHONE: (416) 863-2653		
REFERENCE/DO LECOMMUNICAT	; TE	
TRATION NUMBER: 36,424		
ATTORNEY/AGENT INFORMATION: NAME: Hunt, John C.	v.	
FILING DATE: June 21, 1996	•• •	
PLICATION DATA:		
APPLICATION NUMBER: U5/08/124,400B FILING DATE: October 1, 1996	٠. ٠.	
ATA:		
MS-DOS	·. ··	
, IBM PC compatible	•••	
1/2 inch. 1 4 Mh	 Ω	
~ ⊂ 3	•• ••	
: Toronto		
STREET: Box 25, Commerce Court West		
PONDENCE ADDRESS:	 O	
TITLE OF INVENTION: RETINGIA METADOLIZING PROTEIN	· · ·	
f: Beckett, Barbara R., Jones, Gle		
GENERAL INFORMATION: APPLICANT: Petkovich, P. Martin, White, Jay A.,	; GE 2	
o. 6063606	; Pate	
-U8-724-466B-4 Sequence 4, Application US/08724466B	: Sequ	
	S	
447 FAKILLKIFTVELARHCDWOLLNGPPTMKTSPTVYPVDNLP 487	Db	
467 LAKLEMAVFIHHLVLKENWELAEDDQPFAFPFVDFP 502	Qy	
396 YSICDTHDVADIFTNKEEFNPDRFIVPHPEDASRFSFIPFGGGLRSCVGKE 446	В	

밁 Q В Qγ B ρy

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US-08-882-164D-4
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Best Local Similarity
                                                                                                                                                                                                                   Matches 142;
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                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (416) 863-2653 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,164D
FILING DATE: June 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/667,5
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,4
FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIIM TYPE: Diskette, 3 1/2 inch, COMPUTER: COMPAQ, IBM PC compatible OPERATING SYSTEM: MS-DOS 5.1
SOTTWARE: WORD PERFECT
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein
                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Box 2:
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
          118 GILGKWSMLVLVGDMHRDMRSISLNFLSHARLR---TILLKDVERHTLFVLDSWQQ--NS 172
                                                               59
                                                                                                                                                   10 LPLLLLPSL----LSLLLFLILLK------RNRKTRFNLPPGKSGWPFLGETIGYLK 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M5L 1A9
                                                                                                                             LPALLASALCTFVLPLLLFLAAIKLWDLYCVSGRDRSCALPLPPGTMGFPFFGETL----
                                                                                    PYTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIG 117
                                                 -QMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWPASVR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGSELAKLEMAVFIHHLVLKFNWELAE-----DDQPFAFPFVDFP 502
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                                                                                                                                                                                                                                                                                                                                                                   497 amino acids
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"Tyme 1 1996
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Commerce Court West
                                                                                                                                                                                                         16.4%; Score 439; DB 4; 27.0%; Pred. No. 3.7e-35; tive 85; Mismatches 226
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                                                                                                                                                                                                                                              Length 497;
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US-09-615-192A-405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Materials and Methods for TITLE OF INVENTION: Modification of Plant Lice File Reference: 11000.1003c4U CURRENT APPLICATION NUMBER: US/09/815,192A CURRENT FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 08/975,316 PRIOR APPLICATION NUMBER: US 08/975,316 PRIOR APPLICATION NUMBER: US 08/713,000 PRIOR FILING DATE: 1997-01-21 PRIOR APPLICATION NUMBER: US 08/713,000 PRIOR FILING DATE: 1996-09-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FA
SEQ ID NO 405
LENGTH: 529
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 405, Application US/09615192A
Patent No. 6410718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1998-10-09 NUMBER OF SEQ ID NOS: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bloksberg, APPLICANT: Havukkala,
            163
                                               176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             463 AGSELAKLEMAVFIHHLVLKFNWELAE-----DDQPFAFPFVDFP 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 IFSAQDEAKKFTFNLMAKHIMSMDP-----GEEETEQLKKEYVTFMKGVVSAPLNLPGTA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 TILGSGCLSNLHDSSHKQRKKVIMRAFSREALECYVPVITEEVGSS----LEQWLSCGER
VRDEVDTMVRTVAGSEGTAVNIGELVFELTRDIIYRAAFGTSSTEG-QDEFISILQEFSK 221
                                                                                                                                                                                                                                 PMTLLLSVVPLLLFLGLVARLRRKPPF--PPGPRGLPVIGNML-----MMGELTHR
                                                                                                                                                                                                                                                        GGILGKWSMLVLVGDMHRDMRSIS-LNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFS 175
                                                                                                                                                       GLASLAKKYGGIFHLRMGFLHMVAVSSPDVARQVLQVHDGIFSNRPATIAISYLTYDRAD 130
                                                                                                                                                                                            HVS----KYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFE----
                                               AQDEAK - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FastSEQ for Windows Version 3.0
                                                                                -----MAFAHYGPFWRQMRKLCVMKLFSRKR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bloksberg, Leonard N.
                                                                                                                                                                                                                                                                                                                 Conservative 104;
                                                                                                                                                                                                                                                                                                                                  11.3%; Score 302.5; DB 4
21.9%; Pred. No. 1.7e-21;
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                                      ----KFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMK----
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                                                                                                                                                                                                                                                                                                                                                  Length 529;
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                                                                             ----AESWE----S
                                                                                                                                                                                            ----CSYPRSI 116
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LENGTH: 511;
; TYPE: PRT;
; ORGANISM: Liquidambar styraciflua
US-08-991-677-4
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APPLICANT: Chiang, Vincent L
APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer, Richard H
TITLE OF INVENTION: Production of Syringyl Lignin
FILE REFERENCE: 50617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.8%; Score 289; DB 4; Best Local Similarity 22.0%; Pred. No. 3.6e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/08/991,677A CURRENT FILING DATE: 1997-12-16 EARLIER APPLICATION NUMBER: US 60/033,381
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NUMBER OF SEQ ID NOS: 11
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                                                                                                             QLFGAFNIADFIPWLKWVPQGINVRLN------KARGALDGFIDKIIDDH---IQK
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                                        GSKNSEEVDTDMVDDLLAFYGEEAKVSESDD-----
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08948564 Patent No. 6121512 GENERAL INFORMATION:
                                                                                                                                                                                                                      Best Local Similarity Matches 118; Conserv
                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: איט ביי.
CITY: Raleigh
CITY: Raleigh
CITY: No. 6121512th Carolina
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 50
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bennett, Virginia C
REGISTRATION NUMBER: 37,0
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                                  115 SIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVL-----DSW 168
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 TYGPV---WKSL-----RRNMVQNMLSSTRLKE--FRSVRDNAMDKLINRLKDEAE
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PO Box 37428
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VENTION: No. 6121512el Cytochrome P-450 Constructs and
VENTION: Methods of Producing Herbicide-Resistant Transgenic Plant
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22.9%;
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                                                                                                                                                                                                                                           Score 279.5;
Pred. No. 3.
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ches 216;
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APPLICANT: GUIDO, MATCO
APPLICANT: GUIDO, MATCO
TITLE OF INVENTION: GENOTYPING OF HUMAN CYP:
FILE REFERENCE: SEQ-12P
CURRENT APPLICATION NUMBER: US/09/144,367
CURRENT FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/058,612
PRIOR FILING DATE: 1997-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09144367 Patent No. 6432639 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version
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TYPE: PRT
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                                                                                                                                                   SAISIAEDEEWKRLRSLLSPTFTSGKLKEMVPIIAQYGDVLVRNLRREAETGKPVTL---
                                                                                                                                                                                                                                    GDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILG--K 122
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                                        FLIPILEVLNICVFPREVTNFL-RKSVKRMKESRLEDTQKHRV---DFLQL-MIDSQNSK
                                                                  LNLPGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQ 280
                                                                                                                        DSWQQNSIFSA--QDEAKKFTFNLMAKHIMS-MDPGEEETEQLKK-EYV-TFMKGVVSAP 220
                                                                                                                                                                                                                                                                  LIPDLAMETWILLLAVSLVLLYLYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCM---
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                                                                                               ----KDVFGAYSMDVITSTSFGVNIDSLNNPQDPFVENTKKLLRFDFLDPFFLSITVFP
                                                                                                                                                                                                          --FDMECHKKYGKVWGFYDGQQPVLAITDPDMIKTVLVKE--CYSVFTNRRPFGPVGFMK 115
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Length 503;
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US-09-126-420A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 18
LENGTH: 504
TYPE: PRT
ORGANISM: Solanum melongena
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Best Local Similarity
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Patent No. 6376753
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CURRENT FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: 60/054,351
PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 27
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TITLE OF INVENTION: PURIFIED CYTOCHORME P450 CYP76B1 FROM HELIANTHUS
TITLE OF INVENTION: TUBEROSUS AND ITS APPLICATIONS AS BIOCATALYST IN
TITLE OF INVENTION: PARTICULAR FOR THE DEGRADATION OF ENVIRONMENTAL
TITLE OF INVENTION: POLLUTANTS AND FOR ALTERING THE RESISTANCE OF PLANTS
FILE REFERENCE: 03715.0032
                                                       346 RAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFL-HRKALKDVRYKGYDIPSGWK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 LLLLPSLLSLLLFLILLKRRNRKTRFNLPPGKSGWPFLGETIGY-LKPYTATTLGDFMQQ 70
EPNRKFEDS-----DIENLPYMQAVLKESLRLHPPLPFLIPRETIQDTKFMGYDVPKDTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGKWSMLVLVGDMHRDMRSI-SLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IIILPA-----FILFFSQKNTTKSSYRPPGPPGLPIFGNMFELGTEPYKKMAV---LRQ
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                                                                                                                         -----EPAKLSEHEIKIFVLEMFLAGTETTSSSVEWALTELLRHPEAMAKVKTEISQAI 342
                                                                                                                                                                                   LIGWYLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIA
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DURST, FRANCIS
WERCK-REICHART, DANIELE
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; TYPE: PRT
; ORGANISM: Capsicum
US-09-499-302A-2
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TITLE OF INVENTION: INCOMPATIBLE INTERACTION
FILE REFERENCE: 10324/P64443USO
CURRENT APPLICATION NUMBER: US/09/499,302A
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 10
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 2
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                                                                                GGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPNGLP 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDS----WQQNSIF
                                                                                                                 GYNIPFKTRVIVNAWAIGRDPESWDDPESFSPERF - - ENSSVDFLGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPYGEWT-----RQIRKICILELLSAKM-VKFFSSIRQDELSMWVSSIRTMPNFPV 170
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                                                                                                                                                GYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPF
                                                                                                                                                                                  AQAEVRQVLKEKK--GFQQIDLDELK---YLKLVIKETLRMHPPIPLLVPRECMKDTKID
                                                                                                                                                                                                                 LREEHLEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFL-HRKALKDVRYK 395
                                                                                                                                                                                                                                                     VQISITDDN----
                                                                                                                                                                                                                                                                                  VRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEE
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                                                                                                                                                                                                                                                                                                                                                                                                                  SAQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAP-------
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21.5%; Pred. No. 3.9e-18;
tive 100; Mismatches 208
                                                                                                                                                                                                                                                   ---IKSILVDMFSAGSETSSTTIWALAEMMKKPSVLAK
                                                 ----MKFG--LANVGQPLAQLLYHFDRKLP
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                                                             RESULT 15
US-09-126-420A-26
Sequence 26, Application US/09126420A PATENT NO. 6376753
GENERAL INFORMATION:
APPLICANT: BATARD, YANNICK
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RESULT

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SEQ ID NO 17
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Best Local Similarity
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TITLE OF INVENTION: PURIFIED CYTOCHORME P450 CYP76B1 FROM HELIANTHUS
TITLE OF INVENTION: TUBEROSUS AND ITS APPLICATIONS AS BIOCATALYST IN
TITLE OF INVENTION: PARTICULAR FOR THE DEGRADATION OF ENVIRONMENTAL
TITLE OF INVENTION: PARTICULAR FOR ALTERING THE RESISTANCE OF PLA
FILE REFERENCE: 03715.0032
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TYPE: PRT
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LPHNVSP 441
                                                                                                         RWQQQNNGASSSGSGSFSTWGNNY--MPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWE
                                                                                                                                             VLKEQLRLHPPLPLLIPRKAIQDTKFMGYDIPKGTQVLVNAWAIGRDPEYWDNPFEFKPE
                                                                                                                                                                                                                  LAGTETTSSSVEWALTELLRHPQAMAKVKLEILQVIGPNKKFEECDID-----SLPYVQA
                                                                                                                                                                                                                                                    FAGHETSSVAIALAIFFLOACPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQC
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                                                                     RFLE-----
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DURST, FRANCIS
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                                                                       SKVDVKGQNYELIPFGAGRRMCVGLPLGHRMMHFTFGSLLHEFDWE
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Pred. No. 3.9e-18;
0; Mismatches 182
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; ORGANISM: Rattus norvegicus
US-09-126-420A-26
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SOFTWARE: PatentIn Ve
SEQ ID NO 26
LENGTH: 494
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Best Local Similarity
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                                 451 NYMPEGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAE-----DDQPFAFPEVDEP 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LILLVASVAFLSVLVLMSVWKQRKLSGKLPPGPTPLPFIG---NYLQLNTEKMYSSLMKIS 62
                                                                                                                                                                                                                                                                     VRKQRTDDDLLGWVLKHSNLSTE----QILDLILSLLFAGHETSSVAIALAIFFLQACPK 332
                                                                                                     DVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGN 450
                                                                                                                                                                                                                                         YLSRTVSNVISSIVFGDRFDYEDKEFLSLLRMMLGSFQFTATSTGQLYEMFSSVMK----
AFVPFSIGKRYCFGEGLARMELFLFLTNIMQNFCFKSPQAPQDIDVSPRLVGFATIP 484
                                                                                  DTKFREFLLPKGTEVFPMLGSVLKDPKFFSNPNDFNPKHFLDD:
                                                                                                                                                             IEAKVHEE-----IDRVIGRNRQAKYEDRMKMPYTEAVIHEIQRFADMIPMGLARRVTK 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----IFSAQ-DEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVS 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -QRYGPVFTIHLGPRRVVVLCGQEAVKEALVDQAEEFSGRGEQATFDWLFKG----YGVA 117
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Search completed: June 10, 2003, 22:00:01 Job time: 20 secs

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; ORGANISM: Taxus cuspidata
US-10-142-231-92
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US-10-142-231-92
                                                                                                                                                                                                                                                                                                                           Sequence 92, Application US/10142231
Publication No. US20030077796A1
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES AND THEIR USES
FILE REFERENCE: 62773
CURRENT APPLICATION NUMBER: US/10/142,231
CURRENT FILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: 60/165,250
PRIOR APPLICATION NUMBER: 60/165,250
PRIOR FILING DATE: 1999-11-12
NITMARED OF GRO TO NOC. OF
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 92
LENGTH: 486
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Matches 176;
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247
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73 SKYGKIYRSNLFGEP-TIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGD 131
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                                                                                                                                                                             19 LSLLLFLILLKRRNRK-----TRFNLPPGKSGWPFLGETIGYLKPYTATTLGDEMQQHV 72
                                                                                                                                                                                                                        Similarity
                                                                         LQRKLHATAVNILKHETLSSDFMEDIQDIFQAGMRKWEEEGDIPIQHKCNQIVLNLMAKR 199
                                                                                              MHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKH 191
                                                                                                                    LRYGPIFRCSLFGRTRAVVSVDPEFNKYVLQNEGRLFESNALAPFRNLIGKYGLSAVQGE
                                                                                                                                                        LLDLPP-SEEMGHIYKAFDDFVGAVLSFPLNIPGTTYARGIRARGILLKRIHKCIKERR-
                                                   IMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEERKL 251
                                                                                                                                                                                                              Conservative
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35.1%; Pred. No. 2.2e-58;
tive 97; Mismatches 184
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1110 US-09-796-2568-6
1110 US-09-945-301-4
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1110 US-09-945-301-4
1110 US-09-96-31-6
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1110 US-09-993-31-6
1110 US-09-993-31-8
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Length 486; Indels

Gaps

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RESULT 2
US-10-142-231-88
US-10-142-231-88
Sequence 88, Application US/10142231
Publication No. US20030077796A1
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES AND FILE REFERENCE: 62773
CURRENT APPLICATION NUMBER: US/10/142,231
CURRENT FILING DATE: 2002-05-08
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Best Local :
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SEQ ID NO 88
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PRIOR APPLICATION NUMBER: 60/165,250
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 95
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TYPE: PRT
ORGANISM: Taxus cuspidata
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     LPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGS
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                                                                            RAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKV
                                                                                                                                                                                                                         ALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWV
                                                                                                                                                                                                                                                                                                                                                                                                            QQFIEERMSKFGDVFKTSIIGHPTVVLCGPAGNRLVLSNENKLVQMSWPSSMMKLIGEDC 123
                                                        STKME-GE-EIAWKDLKEMKYSWQVVQETLRMYPPIFGTFRKAITDIHYNGYTIPKGWKL
                                                                                                                                                             L-----KHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIA 345
                                                                                                                                                                                                                                                                                                                                         LGGKTGEQHRIVRAALTRFLGPQALQNHFAKMSSGIQRH----INEKWKGKDEATVLPLVK
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                                                                                                                            LTFTDERGNSLADKEILDNFSMLLHGSYDSTNSPLTMLIKVLASHPESYEKVAQEQFGIL
                                                                                                                                                                                                NSIFSAQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHK 230
                                                                                                                                                                                                                                                                                                                                                                          MLVLVGDMHRDMRSISLNFLSHARLRTILLK---DVERHTLFVLDSWQ------Q
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RESULT 4
US-10-142-231-90
; Sequence 90, Application US/10142231
; Publication No. US20030077796A1
; GENERAL INFORMATION:
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US-10-142-231-64
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Publication No. US20030077796A1
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 64
LENGTH: 497
TYPE: PRT
ORGANISM: Taxus cuspidata
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/142,231
CURRENT FILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: 60/165,250
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 QHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLV 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                             FIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVL----KHSN
                                                                                                                            VHHFVKNFSSYIPVDPNEKVLSDPLPPLPANGFSIKL 493
                                                                                                                                                           IHHLVLKFNWELAED -- DQPFAFPFVDFP-NGLPIRV 509
                                                                                                                                                                                                                               NSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVF
                                                                                                                                                                                                EEYFPEPEEFRPSRFEDEGRHVTP-----YTYVPFGGGLRTCPGWEFSKIEILLF
                                                                                                                                                                                                                                                                                                                                                                    LSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDMHRDMRSISLNFLSHARLRTIL---LKDVERHTLFVLDSWQQNSIFSAQDEAK-----
                                                                                                                                                                                                                                                                   ISWKDLKSMKYTWQAVQESLRMYPPVFGIFRKAITDIHYDGYTIPKGWRVLCSPYTTHLR
                                                                                                                                                                                                                                                                                                                                       LTDQGILDNFSAMFHASYDTTVAPMALIFKLLYSNPEYHEKVFQEQLEIIGNKKE-GE-E
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RESULT 5
US-10-142-231-67
US-10-142-231-67
Sequence 67, Application US/10142231
Publication No. US20030077796A1
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES AND FILE REFERENCE: 62773
CURRENT APPLICATION NUMBER: US/10/142,231
CURRENT FILING DATE: 2002-05-08
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
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US-10-142-231-90
                             NUMBER OF SEQ ID NOS: 95
SOFTWARE: PATENTIN VEY. 2.1
SEQ ID NO 67
LENGTH: 509
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/165,250
PRIOR FILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/142,231 CURRENT FILING DATE: 2002-05-08
           TYPE: PRT
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TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES AND THEIR USES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGQDTTASALATILKHLSLSPHLLQRLRKE-CEKLRDNKEAG-GPLTWSEIKSVGYLHN 362
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US-10-142-231-65
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Best Local Similarity
                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(507)
OTHER INFORMATION: "Xaa
                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 95
                                 158;
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; ORGANISM: Taxus cuspidata US-10-142-231-67
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SEQ ID NO 65
LENGTH: 507
TYPE: PRT
ORGANISM: Taxus cuspidata
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Publication No. US20030077796A1
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES
FILE REFERENCE: 62773
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/142,231
CURRENT FILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: 60/165,250
PRIOR FILING DATE: 1999-11-12
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10 LPLLLLPSLLSLLLFLILLKRRNRKTRENLPPGKSGWPFLGETIGYLKPYTATTLGDFMQ 69
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                                                       Conservative
                                                                                                                                         (507)
ON: "Xaa" equals any peptide
                                                                        21.8%;
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                                                                        Score 585;
Pred. No. 1
                                                    Mismatches
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..8e-39;
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RESULT 7
US-10-142-231-57
US-10-142-231-57; Sequence 57, Application US/10142231; Publication No. US20030077796A1; GENERAL INFORMATION:
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US-10-142-231-57
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 57
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TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES AND THEIR USES
FILE REFERENCE: 62773
CURRENT APPLICATION NUMBER: US/10/142,231
CURRENT FILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: 60/165,250
PRIOR APPLICATION NUMBER: 60/165,250
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 484
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                                                                                                                                                                                                                                                                  Similarity
                                                                     KWSMLVLVGDMHRDMRSISLNFLSHARLRTILLK---DVERHTLFVLDSWQQNSIFSAQD
                                                                                                                                          TTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILG
                                                                                                                                                                                                 EHHTLLPLLLLPSLLSLLLFLILL----KRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTA
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     EAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATI 238
                                       QDSVLGKIGEEHRIVRTALARCLGPQALQNYVSKMSSEIQRH---INQKWKGKGEVKMLP
                                                                                                                                                                          EMDTFVQLESSPVLLSLTLTLILLFIFCSKQYRSSLKLPPGNMGFPLIGETIA----LAS
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29.3%;
                                                                                                                                                                                                                                                94; Mismatches
                                                                                                                                                                                                                                                                Score 583; DB 9;
Pred. No. 2.4e-39;
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CURRENT FILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: 60/165,250
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 58
LENGTH: 501
TYPE: PRT
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Publication No. US20030077796A1
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES
FILE REFERENCE: 62773
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   DDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSR 418
                                                                                                                                                                                                      FNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIER
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                                       EILDNESEMLHASYDT-TVSPTVCIFKLLSANPECYEKVVQEQLGILGNKKD-GE-EMCW
                                                                                                                                          KMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVL-----KHSNLSTE
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Best Local
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SEQ ID NO 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/142,231
CURRENT FILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: 60/165,250
PRIOR FILING DATE: 1999-11-12
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TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES
FILE REFERENCE: 62773
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                                                                                                                                                                                                        WQVVQETLRMFPPLFGSFRKAMVDINYDGYTIPKGWIVLWTTYSTHVKEEYFNEPGKFRP
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                                                                                                                                                                                                                                                                                                                          LLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFT 367
                                                                                                                                                                                                                                                                                                                                                                                                      IKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSN-----LSTEQILDLILS
                                                                                   AED--DQPFAFPFVDFP-NGLPIRV 509
                                                                                                                                                               WRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWEL 487
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                                                                                                                                                                                                                                                                                                                                                                 -----GKASSNQDLLSVLLSFKDERGNPLRDEEILDNFSL
                                                                                                                          -YTFLPFGGGLRTCPGWEFSKTEILLFIHHFVKTFGSYL
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US-10-142-231-56
; Sequence 56, Application US/10142231
; Publication No. US20030077796A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES ANI
; FILE REFERENCE: 62773
; CURRENT APPLICATION NUMBER: US/10/142,231
; CURRENT APPLICATION NUMBER: 60/165,250
; PRIOR APPLICATION NUMBER: 60/165,250
; PRIOR FILING DATE: 1999-11-12
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Publication No. US20030077796A1
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES
FILE REFERENCE: 62773
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CURRENT FILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: 60/165,250
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 59
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                               QKDIYFKQPDKFMPSRFEEED-----GHLDAY--TFVPFGGGRRTCPGWEYAKVEIL
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Pred. No. 3.9e-38;
)3; Mismatches 195;
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407 413 348 353 289 295 Gaps

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; LENGTH: 484
; TYPE: PRT
; ORGANISM: Taxus cuspidata
US-10-142-231-56
; NAME/KEY: misc_feature; LOCATION: (1)..(500)
; OTHER INFORMATION: "Xaa" equals any peptide US-10-142-231-61
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US-10-142-231-61
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                                                                                                               SEQ ID NO 61
LENGTH: 500
TYPE: PRT
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/142,231
CURRENT FILING DATE: 2002-05-08
                                                                                                                                                                                                                                                                                                          APPLICANT: Croteau, Rodney et al. TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 56
                                                                                                                                                                       NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/165,250 PRIOR FILING DATE: 1999-11-12
                                                                           ORGANISM: Taxus cuspidata FEATURE:
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Pred. No. 8.6e-38;
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US-10-142-231-62
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PRIOR PILLAGIION NUMBER: 60/165,250
PRIOR FILLING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 62, Application US/10142231
Publication No. US20030077796A1
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES AND THEIR USES
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Best Local Similarity
                                                                                                                                                       Matches
                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/142,231 CURRENT FILING DATE: 2002-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 62773
                                                                                                                                                                                                                                                                     LENGTH: 48
                                                                                                                                                                                                                                                   ORGANISM: Taxus cuspidata
                                                                                                                                                                         Local Similarity
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 QPPQKFLNERGKKFGPVFKTSLIGHPTVVLCGSSGNRFLLSNEEKLVRMSLPNSYMKLLG
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                                                                         TLIQIQSSPDELSFTLTAFLGVVVLLIFRYKHRSALKLPPGNLGLPFIGETI----TFAS
                                                                                                             TLLPLLLLPSLLSLLL-----FLILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGEEHRILRAALARFLRPQALQGYVAKMSSEIQHH----IKQKWKGNDEVKVLPLIRTLIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKFNWELAED--DQPFAFPFVDFP-NGLPIRV 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EADKFMPSRFEEGKYVAPYT------FLPFGAGLRVCPGWEFAKTEILLFVHHFI 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVL
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                                                                                                                                                       Conservative
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                                                                                                                                                   91;
                                                                                                                                                                       Score 558.5; DB 9; Pred. No. 2.4e-37;
                                                                                                                                                       Mismatches
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RESULT 14

US-10-142-231-87

i Sequence 87, Application US/10142231

i Publication No. US20030077796A1

i GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: CYTOCHROME P450 OXYGENAS

FILE REFERENCE: 62773

CURRENT APPLICATION NUMBER: US/10/142,231

CURRENT APPLICATION NUMBER: 05-08

PRIOR APPLICATION NUMBER: 60/165,250

PRIOR FILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 95
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; ORGANISM: Taxus cuspidata
US-10-142-231-87
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                                                246 MEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLG-WVL----KHSNLSTEQ
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                                                                                      IATSLFFGVNDDGER--ERLHDLLETALAGVFSIPLDFPGTNYRKALEARLKLDKVLSSL
                                                                                                                                                                                               GDMHRDMRSISLNFLSHARLRTILLK---DVERHTLFVLDSWQQNSIFSAQDEAKKFTFN 186
                                                                                                                                                                                                                                                                  QHYSKYGKIYRSNLFGEPTIYSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLYLV 129
                                                                                                                                                                                                                                                                                                                                         LPLLLLPSLLSLLLFLILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDEWQ
                                                                                                               LMAKHIMSM-DPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERK 245
                                                                                                                                                             GEKHRILRAAVNRYLGPGALQNYMAKMRSEIEHH----MNEKWKGKEQVKVLPLVKENVFS
                                                                                                                                                                                                                                      ERQKKFGSVFKTSLIGDRTVVLCGFSGNRLLLSNENKLVEASWFSSSIKLIGEDSIAGKN 146
                                                                                                                                                                                                                                                                                                                  LSVTITVTAIAVITLLLVLIRSKPQSCVNLPPGKLGYPFIGETLQLLQAFRSNRPQQFFD
                        IERRRSDLRSGVASGNE - - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KWSMLVLVGDMHRDMRSISLNFLSHARLRTILLK---DVERHTLFVLDSWQQNSIFSAQD 178
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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CYTOCHROME P450 OXYGENASES
                                                                                                                                                                                                                                                                                                                                                                                                                   20.8%; Score 558.5; DB 9; 27.9%; Pred. No. 2.6e-37;
                                                                                                                                                                                                                                                                                                                                                                                                       108;
                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 210;
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US-10-142-231-91
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SEQ ID NO 91
LENGTH: 498
TYPE: PRT
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Publication No. US20030077796A1
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES AND THEIR USES
FILE REFERENCE: 62773
CURRENT APPLICATION NUMBER: US/10/142,231
CURRENT FILING DATE: 2002-05-08
PRIOR APPLICATION UNMBER: 60/165,250
PRIOR PRICE DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 95
CORDENADE: DESCONTO IN 1999-11-12
NUMBER: DESCONTO IN 1999-11-12
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                                  QQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFN 484
                                                                                                         NETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQ 431
                                                                                                                                               SYDTTTSPMALIFKLLSSNPECYQKYVQEQLEIL-SNKEEGE-EITWKDLKAMKYTWQVA
                                                                                                                                                                                 GHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVI 371
                                                                                                                                                                                                                        SLDRQQPRRICSLFCSLSEMTKG------LPH---PMDEILDNFSSLLHA
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        QEGKHVAP - - -
                                                                      QETLRMFPPVFGTFRKAITDIQYDGTNSKRG-KLLWTTYSTHPKDLYFNEPEKFMPSRFD
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                                                                                                                                                                                                                                                            KEEDQEEEEVKTE--DEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFA
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29.6%; Pred. No. 6.4e-37;
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Search completed: June 10, 2003, 22:03:35 Job time : 33 secs

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Result
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Maximum Match 1008
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Maximum DB seq length: 2000000000
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21 US-09-791-537-67246

18 US-09-464-535-36

21 US-09-708-427-51512

21 US-09-708-427-51511
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Sequence 2, Appli
Sequence 67246, A
Sequence 36, Appl
Sequence 51512, A
Sequence 51511, A
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LENGTH: 513
TYPE: PRT
                                                                                                                                                                                                                                                     Sequence 2, Application PC/TUS0003820

GENERAL INFORMATION:

APPLICANY: THE ARIZONA BOARD OF REGENTS ON BEHALF OF THE UNIVERSITY OF ARIZONA

TITLE OF INVENTION: DWF4 POLYNCCLEOTIDES, POLYPEPTIDES AND USES THEREOF

FILE REFERENCE: 2225-0001.40

CURRENT APPLICATION NUMBER: PCT/US00/03820

CURRENT FILING DATE: 2000-02-11

EARLIER APPLICATION NUMBER: 60/119,657

EARLIER FILING DATE: 1999-02-11

EARLIER FILING DATE: 1999-02-11

EARLIER FILING DATE: 1999-02-11

EARLIER FILING DATE: 1999-02-11

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.0
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nes 513; Conserv
Score 2681; DB 1;
Pred. No. 3.4e-231;
0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: AZPIROZ, Ricardo
APPLICANT: CHOE, Sunghwa
APPLICANT: FELDMANN, Kenneth
TITLE OF INVENTION: DWF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: 2225-0001
                                                                                                                                                                                                                                                                  SEQ ID NO 2
                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/502,426
CURRENT FILING DATE: 2000-02-11
EARLIER APPLICATION NUMBER: 60/119,657
EARLIER FILING DATE: 1999-02-11
EARLIER APPLICATION NUMBER: 60/119,658
EARLIER FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
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TYPE: PRT
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Pred. No. 3.4e-231;
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THERE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
TITLE OF INVENTION: METHODS OF USE THEREOF
TILE REFERENCE: 261/210
CURRENT APPLICATION UMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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YKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYD
                                  ILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDD
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Pred. No. 7.8e-231;
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RESULT 5
US-09-708-427-51512
; Sequence 51512, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
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US-09-464-535-36
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CURRENT FILING DATE: 1999-12-15
EARLIER APPLICATION UNMBER: 60/112,555
EARLIER FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Microsoft Office 97
SEQ ID NO 36
LENGTH: 392
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APPLICANT: McGonigle, Brian
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: STEROL BIOSYNTHETYC ENZYMES
FILE REFERENCE: BB1306 US NA
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70.3%;
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Pred. No. 2.9e-125;
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RESUL7 6
US-09-708-427-51511
Sequence 51511, Application US/09708427
GENERAL INFORMATION:
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APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Xaa is NAME/KEY: misc_feature LOCATION: 1..484
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Conservative 10
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Pred. No. 1.2e-81
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                                                                                                                                                                                                                                                                Sequence 51510, Application US/09708427 GENERAL INFORMATION: APPLICANT: N. ALEXANDROV et al.
                                                                                           CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 51510
LENGTH: 542
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                                                                                                                                                                                                          TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
                                        ORGANISM: Zea mays subsp. FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: 1..485
OTHER INFORMATION: Xaa is
     NAME/KEY: misc_feature
LOCATION: 1..542
                                                                               TYPE: PRT
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Pred. No. 1.2e-81;
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                                                                                                            SEQ ID NO 2
LENGTH: 472
                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09306844
GENERAL INFORMATION:
APPLICANT: KONCZ, Csaba
APPLICANT: Mathur, Jaideep
Query Match
Best Local Similarity
                                                                                                                                              TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING CYTOCHROME P450-TYPE TITLE OF INVENTION: PROTEINS INVOLVED IN THE BRASSINOSTEROID SYNTHESIS IN TITLE OF INVENTION: PLANTS FILE REFERENCE: 147-186 CURRENT APPLICATION NUMBER: US/09/306,844 CURRENT FILING DATE: 1999-05-06 EARLIER APPLICATION NUMBER: 08/622,166 EARLIER FILING DATE: 1996-03-27 NUMBER OF SEQ ID NOS: 12 SOFTWARE: Patentin Ver. 2.0
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Matches 213; Conserva
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Best Local 9
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APPLICANT: Altmann, Thomas
                                                                                               TYPE:
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Pred. No. 1.4e-81;
 978.5; DB 17;
No. 2.7e-78;
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                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                           NAME/KEY: UNSURE
LOCATION: 1..472
OTHER INFORMATION: any n or Xaa = unknown
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                                 72 VSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGD 131
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VARYGSVFWTHLFGEPTIFSADPETNRFVLQNEGKLFECSYPASICNLLGKHSLLLMKGS 123
                                                                                                     LLLLPSLLSLLLFLILLKRRNRKTRENLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQH
                                                                     LLLLSSIAAGFL---LLLRRTRYRRMGLPPGSLGLPLIGETFQLIGAYKTENPEPFIDER
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Pred. No. 2.7e-78;
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US-09-513-996A-56469
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APPLICANT: N. ALEXANDROV et al.
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 56469
LENGTH: 472
TYPE: PRT
                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: ENCODED THEREBY FILE REFERENCE: 2750-709P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 81028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: UNSURE
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OTHER INFORMATION: any n or xaa = unknown
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                                       192 IMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEERKL 251
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                                                                                                                                                                                                                                                                                               h 36.5%; Score 978.5; DB 19;
Similarity 41.9%; Pred. No. 2.7e-78;
10: Conservative 79; Mismatches 171;
                                                                             LHKRMHSLTMSFANSSIIKDHLMLDIDRLVRFNLDSWSSRVLL--MEEAKKITFELTVKQ
                                                                                                              MHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKH
           LMSFDPG-EWSESLRKEYLLVIEGFFSLPLPLFSTTYRKAIQAR---
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Best Local Similarity
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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TYPE: PRT
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                                                                     VSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGD 131
             NETLRVANIIGGVFRRAMTDVEIKGYKIPKGWKVFSSFRAVHLDPNHFKDARTFNPWRWQ
                                                                                                                                                                                                         VVVMKRREEEEEGAE-
                                                                                                                                                          DIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFA
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                                        NETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQ
                                                                                                                                                                                                                                                                                                         VARYGSVFMTHLFGEPTIFSADPETNRFVLQNEGKLFECSYPASICNLLGKHSLLLMKGS
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                                                                                                                                                                                                                                                                                                                                                                 LLLLSSIAAGFL---LLLRRTRYRRMGLPPGSLGLPLIGETFQLIGAYKTENPEPFIDER
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                                                                                                                                                                                                                                                                                                                                                                                                                          36.5%; Score 978.5; DB 2
41.9%; Pred. No. 2.7e-78;
tive 79; Mismatches 171
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RESULT 13
US-09-935-625-5735
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Sequence 5227, Application US/09
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
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SEQ ID NO 5227
LENGTH: 472
TYPE: PRT
ORGANISM: Arabidopsis t
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CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                        DKLVFFPTTRTQKRYPIFVKR
                                                                                                             GYETTSTIMTLAVKFLTETPLALAQLKEEHEKIRAMKSD--SYSLEWSDYKSMPFTQCVV
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                                                                                   DOPFAFPFVDFPNGLPIRVSR
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Pred. No. 2.7e-78;
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RESULT 14
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                                                                                                                Sequence 7739, Application US/09935625
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 5735
LENGTH: 472
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
          NUMBER OF SEQ ID NOS: SEQ ID NO 7739
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GENERAL INFORMATION:
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                          TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, TITLE OF INVENTION: MODULATING VARIOUS RESPONSES FILE REFERENCE: 2750-1481P CURRENT APPLICATION NUMBER: US/09/935,625 CURRENT FILING DATE: 2001-08-24 NUMBER OF SEQ ID NOS: 33136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: N. ALEXANDROV et al.
LENGTH: 472
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RESULT 15
US-09-935-625-9349
Sequence 9349, Application US/09935625
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
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                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 9349
LENGTH: 472
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Best Local S
Matches 210
     Best Local Similarity Matches 210; Conserv
                                   Query Match
                                                                                                                                                                                                                                                              TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, TITLE OF INVENTION: MODULATING VARIOUS RESPONSES FILE REFERENCE: 2750-1481P
                                                                                   NAME/KEY: peptide LOCATION: 1..472 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                    FEATURE:
                                                                                                                                                                    TYPE: PRT
                                                                                                                                                  ORGANISM: Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LMSFDPG-EWSESLRKEYLLVIEGFFSLPLPLFSTTYRKAIQAR-----RKVAEALT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LHKRMHSLTMSFANSSIIKDHLMLDIDRLVRFNLDSWSSRVLL--MEEAKKITFELTVKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLLLSSIAAGFL---LLLRRTRYRRMGLPPGSLGLPLIGETFQLIGAYKTENPEPFIDER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              DQPFAFPFVDFPNGLPIRVSR 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQNNGASSSGSGSFSTWGNN-YMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAED
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                    36.5%;
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     79;
Score 978.5; DB 23;
Pred. No. 2.7e-78;
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     Indels
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	DKLVEEPTTRTQKRYPIEVKR 467	447	В
	DQPFAFFFVDFPNGLPIRVSR 511	491	δ
446	SNSVTTGPSNVFTPFGGGPRLCPGYELARVALSVFLHRLVTGFSWVPAEQ	397	밁
490	QQNNGASSSGSGSFSTWGNN-YMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAED	432	δ
396	NETLRVANIIGGVFRRAMTDVEIKGVKIPKGWKVFSSFRAVHLDPNHFKDARTFNPWRWQ	337	В
431		372	δ
336	GYETTSTIMTLAVKFLTETPLALAQLKEEHEKIRAMKSDSYSLEWSDYKSMPFTQCVV	279	ф
371	GHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVI	. 312	Ϋ́
278	VVVMKRREEEEEGAERKKDMLAALLAADDGFSDEEIVDFLVALLVA	233	밁
311	DIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFA	252	δ
232	LMSFDPG-EWSESLRKEYLLVIEGFFSLPLPLFSTTYRKAIQARRKVAEALT	182	Вb
251	IMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEERKL	192	δĀ
181	LHKRMHSLTMSFANSSIIKDHLMLDIDRLVRFNLDSWSSRVLLMEEAKKITFELTVKQ	124	망
191	MHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKH	132	οy
123	VARYGSVFMTHLFGEPTIFSADPETNRFVLQNEGKLFECSYPASICNLLGKHSLLLMKGS	64	₽
131	VSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGD	72	ΔĀ
63	LLLSIAAGFLLLLRRTRYRRMGLPPGSLGLPLIGETFQLIGAYKTENPEPFIDER 63	7	Db
71	12 LLLLPSLLSLLLFLILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFWQQH 71	12	Qy

Search completed: June 10, 2003, 22:02:53 Job time: 163 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd
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US-10-424-599-18693
US-09-502-426A-19
US-10-424-599-178693
US-09-502-426A-25
US-10-395-463-24
US-09-502-426A-25
US-10-395-6153-92
US-10-310-154-384
US-09-502-426A-25
US-10-310-154-383
US-10-425-114-5905
US-09-502-426A-20
US-10-310-154-381
US-10-425-114-64364
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US-10-425-114-57231	US-10-356-153-91	US-10-356-153-87	US-10-356-153-62	US-10-424-599-205981	US-10-356-153-61	US-10-356-153-56	US-10-356-153-59	US-10-424-599-248036	US-10-356-153-89	US-10-356-153-58	US-10-356-153-57	US-10-356-153-65	US-10-356-153-67	US-10-356-153-90	US-10-424-599-275182	US-10-356-153-64	US-10-356-153-88	US-10-310-154-382
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ALIGNMENTS

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301 ILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDD 360	241 FIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQ 300 241 FIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQ 300		1 MFETERHTLLPLLLLPSLLSLLLELILLKRRNRKTRENLPPGKSGWPELGETIGYLKPYT 60 	Whatch 100.0%; Score 2681; DB 5; Length 513; Local Similarity 100.0%; Pred. No. 8.2e-252; Local Similarity 0; Mismatches 0; Indels 0; Gaps 0; Local Similarity 0; Mismatches 0; Length 513; Conservative 0; Mismatches 0; Length 513; Leng	SULT 1 1-09-502-426A-2 1-09-502-426A Sequence 2, Application US/09502426A GENERAL INFORMATION: APPLICANT: AZPIROZ, Ricardo APPLICANT: EHDMANN, Kenneth TITLE OF INVENTION: DWF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF FILE REFERENCE: 225-0001 CURRENT FILING DATE: 2000-02-11 PRIOR APPLICATION NUMBER: US/09/502,426A CURRENT FILING DATE: 1999-02-11 PRIOR PHILIATION NUMBER: 60/119,657 PRIOR PHILIATION NUMBER: 60/119,658 PRIOR FILING DATE: 1999-02-11 PRIOR APPLICATION NUMBER: 60/119,658 PRIOR FILING DATE: 1999-02-11 NUMBER OF SEQ ID NOS: 25 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 513 TYPE: PRT ORGANISM: Arabidopsis sp09-502-426A-2
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APPLICANT: AZDITOZ, Ricardo
APPLICANT: Choe, Sunghwa
APPLICANT: Feldmann, Kenneth A.
TITLE OF INVENTION: DWF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: 11696-070001
CURRENT APPLICATION NUMBER: US/09/502,426B
CURRENT FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/119,657
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: US 60/119,658
PRIOR FILING DATE: 1999-02-11
NUMBER OF SEO ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 513
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-502-426B-2
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Matches 513; Conserv
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QPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLV 480
                                                                                                           FIERKMEERKLDIKEEDQEEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQ
                                                                                                                                                                                                                                     KKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILK
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                                                                                                                                                                FIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQ
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Pred. No. 8.2e-252;
0; Mismatches 0;
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US-10-395-463-2
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Best Local Similarity
Matches 343; Conserv
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LENGTH: 506
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APPLICANT: Sakamoto, Tomoaki
APPLICANT: Iwahori, Shuichi
APPLICANT: Iwahori, Shuichi
TITLE OF INVENTION: Method of Controlling Character of Monocotyledon by Modifica
TITLE OF INVENTION: Overexpression of Cytochrome P450 Monocoygenase Gene Involvation: Biosynthesis and Monocotyledon Modified by the Gene
FILE REFERENCE: 59150-8022
CURRENT APPLICATION NUMBER: US/10/395,463
CURRENT FILING DATE: 2003-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: JP 2002-276398
PRIOR FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
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WEDYKEMVFTQCVINETLRLGNVVRFLHRKVIKDVHYKGYDIPSGWKILPVLAAVHLDSS
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                                                                                                                      RYDOPNLENPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIH
                                                                                                                                                                                                        KEQILDLLLSLLFAGHETSSMALALAIFFLEGCPKAVQELREEHLGIARRQRLRGECKLS
                                                                                                                                                                                                                   TEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELN
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 ; OTHER INFORMATION: Clone ID: UC-ZMROB73080G04_FLI.pep US-10-425-114-72982
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Best Local Sim
Matches 234;
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LENGTH: 300
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
FILE REFERENCE: MININERD: NC/10/424.599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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                               ORGANISM: Zea mays FEATURE:
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Zhou Yihua
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Pred. No. 8.1e-105;
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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molec
TITLE OF INVENTION: Plants and Uses There
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILLING DATE: 2003-04-28
RUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Clone ID: PAT_MRT3847_132377C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Glycine
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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KEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHS-NLSTEQILDLILSLLFAG 312
                                                                                                                                                     RYGPIFTTHVFGEPTVFSADPETNRFILLNEGKLFECSYPGSISNLLGKHSLLLMKGSLH 136
                                                                                                                                                                                                                       PELFLLIISAVLLFPHRRSRCRRFRLPPGTLGLPLVGETLQLISAYKSDNPEPFMDQRVK 76
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                                                           SMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEERKLDI 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KFNWELAEDDQPFAFPFVDFPNGLPIRVSRI 512
                               SFDPG-EWTETLRKEYVLVIEGFFSVPLPLFSSTYRRAIKARTKVAEALTLVVRDRR---
                                                                                            KRMHSLTMSFANSSIIKDHLLVDIDRLIRLNLDSWSDRVLL--MEEAKKITFELTVKQLM
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67.1%;
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Pred. No. 1
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372 NETLRIGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQ : : : :	Qy 312 GHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVI 371 : : : : : : : : : : : : :	Qy 252 DIKEEDQEEEEVKTEDEAEMSKSDHYRKQRTDDDLLGWYLKHSNLSTEQILDLILSLLFA 311 : : :	Qy 192 IMSMDDGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEERKL 251 : : :	Qy 132 MHRDMRSISLNELSHARLRTILLKDVERHTLEVLDSWQQNSIFSAQDEAKKFTFNLMAKH 191 : : : : : : : : : : - - -	Oy 72 VSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGD 131 :: :: ::	ETIGYLKPYTATTLGI ; ETFQLIGAYKTENPEE	Query Match 36.5%; Score 978.5; DB 5; Length 472; Best Local Similarity 41.9%; Pred. No. 3.2e-86; Matches 210; Conservative 79; Mismatches 171; Indels 41; Gaps 8;	ENGTH: PE: PR RGANISM 502-42	FILING DATE: 1999-02-11 R OF SEQ ID NOS: 25 ARE: FastSEQ for Windows Ver NO 19	CURRENT FILING DATE: 2000-03-102, 450A CURRENT FILING DATE: 2000-03-11 PRIOR APPLICATION NUMBER: 60/119,657 PRIOR FILING DATE: 1999-02-11 PRIOR APPLICATION NUMBER: 60/119,658	EOTID	; Sequence 19, Application US/09502426A ; GENERAL INFORMATION: ; APPLICANT: AZPEIROZ, Ricardo ; APPLICANT: CHOE, Sunghwa	SULT 7 -09-502-426A-19	Qy 493 PFAFPFVDFPNGLPIRVSR 511	Db 408 SNSEASSPGNVYTPEGGGPRLCPGYELARVYLSVELHRIVTRYSWEPAEEDK 459		373 ETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDDPNLFNPWRWQQ	QY 313 HETSSVAIALAIFELQACPKAVEELREBHLEIARAKKELGESELNWDDYKKMDETQCVIN 372 ON THE STATE OF THE STA	Db 251 KESVTEEKKNDMLGALLASGYHFSDEEIVDFMLALLVAG 289
Qy 491 DQPFAFPEVDEPNGLPIRVSR 511	QY 432 QQNNGASSGSGSFSTWGNN-YMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAED 490	3/2 NETERLGNYKFELHKKALKDYKYKGYDIPSGWYLPVISAVHLDNSKYOQPNLENEWKWQ	312 GHETSSVALALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWIDDYKKMDFTQCVI	252 DIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDLLGWVLKHSNLSTEQILDLILSLLFA ::: ::: 233 VVVMKRREEEEEEGAE	192 IMSMDPGEEETEOLKKEYVTEMKGVVSAPLALGTAYHKALQSRATILKFIERKMEERKL	132 MHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKH	Qy 72 VSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGD 131	Qy 12 LLLLPSLLSLLLFLILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQOH 71 : : :	Ouery Match 36.5%; Score 978.5; DB 5; Length 472; Best Local Similarity 41.9%; Pred. No. 3.2e-86; Matches 210; Conservative 79; Mismatches 171; Indels 41; Gaps 8;	; LENGTH: 4/2 ; TYPE: PRT ; ORGANISM: Arabidopsis thaliana US-09-502-426B-19	Z R		FILING DATE:	222.	NESULE 6 US-09-502-426B-19 ; Sequence 19, Application US/09502426B . GENERAL INFORMATION:		Qy 491 DQPFAFPFVDFPNGLPIRVSR 511		Db 337 NETLRVANIIGGVFRRAMTDVEIKGYKIPKGWKVFSSFRAVHLDPNHFKDARTFNPWRWQ 396

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US-09-502-426A-25
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US-10-395-463-24
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            Sequence 25, Application US/09502426A GENERAL INFORMATION:
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CURRENT FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: JP 2002-276398
PRIOR FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 24
LENGTH: 501
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Best Local
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   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tanaka, Hiroshi
APPLICANT: Kayano, Toshial
APPLICANT: Matsuoka, Makoi
APPLICANT: Sakamoto, Tomoi
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AZPIROZ,
                                                                                                                                                  IHHLVLKFNWELAEDDQPFAFPFVDFPNGLPIRVSRIL 513
                                                                                                                                                                                                          NSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVF 475
                                                                                                                                                                                                                                                        LNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLD
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                                                                                                                    LHHLVTRFSWEETEEDRLVFFPTTRTLKGYPINL~RLL 496
                                                                                                                                                                                    NEHYENARTFNPWRWQINNKLQNAVGA-----NIFTPFGGGPRLCPGYELARVVVSIF
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Sakamoto, Tomoaki
Iwahori, Shuichi
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Ricardo
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RESULT 11 US-09-502-426B-25

Sequence 25, Application US/09502426B GENERAL INFORMATION:

APPLICANT: Azpiroz, Ricardo APPLICANT: Choe, Sunghwa

APPLICANT:

Feldmann,

Kenneth

OF INVENTION: DWF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: CHOE, Sunghwa
APPLICANT: FELDMANN, Kenneth
TITLE OF INVENTION: DWF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: 2225-0001
FILE REFERENCE: 2225-0001
CURRENT APPLICATION NUMBER: US/09/502,426A
CURRENT FILING DATE: 2000-02-11
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NUMBER OF SEQ ID NOS: 25
SOFTMARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/119,657 PRIOR FILING DATE: 1999-02-11
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OTHER INFORMATION: Consensus sequence
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TYPE: PRT
ORGANISM: Artificial Sequence
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KELAKLEMXVFLHRLVQXF-WELAXXXD-XXXKLVXFPTXRPXDNLPIKV 565
                                   SELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFP----NGLPIRV 509
                                                                                                     VLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAG
                                                                                                                                               XRAKKXXXESXLTXXDYKKMXYTXCVINETLRLAXIVGGXFRXAXKDVEINGYXIPKGWK
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                                                                                                                                                                                  ARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWK 404
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                                                                        VXYSIRAVHLDPDXYPDPEKFNPXRWXXKXXXXSNSXXXXXXXXXXXXPFGGGPRLCPG
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Pred. No. 1.7e-73;
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RESULT 12
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CURRENT APPLICATION NUMBER: US/09/502,426B
CURRENT FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/119,657
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: US 60/119,658
PRIOR FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                    Sequence 384, Application:
            APPLICANT:
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OTHER INFORMATION: CONS
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(575)
OTHER INFORMATION: Xaa
                                        APPLICANT: Edgerton, Michael APPLICANT: Chomet, Paul S. APPLICANT: Adams, Thomas H APPLICANT: Ruff, Thomas G.
APPLICANT:
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TYPE: PRT
ORGANISM: Artificial Sequence
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           Agarwal, Ameeta K.
Ahrens, Jeffrey E.
Ball,
                                                                                                                    Application US/10310154
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Pred. No. 1.7e-73;
5; Mismatches 242
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SEQ ID NO 384
LENGTH: 503
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/337,358 PRIOR FILING DATE: 2001-12-04
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                                                                                                                  MLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQ--DEAKK 182
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Zeng, Xiaoping
Zhang, Qiang
Zhao, Yajuan
Zhao, Yajuan
         LKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSNLST
                                                                                                                                                              PFIDERVARHGSGVFTTHVFGERTVFSADPAFNRLLLAAEGRAVSCSYPSSIATLLGPRS
                                       ITFNLTVWQLVSIEPG-PWTESVRREYVKLVDGFFSIPFPFASLLPFTVYGQALKARKKV
                                                                     FTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPLN----LPGTAYHKALQSRATI
                                                                                                 LLLTSGPAHKRLHSLTLTRLGRP-ASPPLLAHIDRLVLATMRGWDRPGAGAMRLLDEAKK
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Luethy, Michael M.
Lund, Adrian
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Deikman, Jill
Deng, Molian
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McKiel, Christine L.
Miller, Philip W.
Padmavathi, Manchikanti
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Bell, Erin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xu, Nanfei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vidya, K.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Galligan, Meghan M
Hinchey, Brenda S.
Huang, Shihshieh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang,
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Laccetti, Lucille
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                                                                                                                                                                                                                                                                                    Conservative
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37.2%;
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                                                                                                                                                                                                                                                                                                  Score 832; DB 6;
Pred. No. 6.2e-72;
                                                                                                                                                                                                                                                                                   Mismatches 191;
                                                                                                                                                                                                                                                                                                                Length 503;
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                   186
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; ORGANISM: Taxus cuspidata
US-10-356-153-92
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US-10-356-153-92
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 92, Application US/10356153 GENERAL INFORMATION:
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CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: US/10/142,231
PRIOR FILING DATE: 2002-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver.
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TITLE OF INVENTION: CYTOCHROME POPILE REFERENCE: 62773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 48
TYPE: PRT
                                                                                                                                         312 GHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFTOCVI 371
                                                                                                                                                                                       258
                                                                                                                                                                                                                                                       200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176;
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          QQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDD
                                                                                                          GVETSAMAMTFAVKYLAENPRALEELRAEHDALLKAKGK-GNEKLTWNDYQSMKFVHCVI 351
                                         NETLRLGGATVVLFREAKQDIKVKDFVIPKGWTVSVFLSATHVDGKYHYEADKFLPWRWQ
                                                                         NETLRIGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQ 431
                                                                                                                                                                                                          DIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSLLLFLILLKRRNRK-----TRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQHV
                                                                                                                                                                                                                                                                                                           LORKLHATAVNLLKHETLSSDFMEDIQDIFQAGMRKWEEEGDIPIQHKCNQIVLNLMAKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 816.5; DB 6
Pred. No. 1.9e-70;
                                                                                                                                                                            -----LRNDLLTKLVREGTFSDEIIADTIIFFVFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6;
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             491
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                                                                         US-10-310-154-383
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US-10-310-154-383
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                                                                                                      PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 383
LENGTH: 518
TYPE: PRT
     Query Match
Best Local Similarity
Matches 160; Conserv
                                                                                                                                                                                               TITLE OF INVENTION: Gene Sequences and Uses FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
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                                                                                        ORGANISM:
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                                                                                        Zea
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zhao, Yajuan
zhou, Li
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Malloy, Kathleen A.
McKiel, Christine L.
Miller, Philip W.
Padmavathi, Manchikanti
Parnell, Laurence D.
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Zeng, Xiaoping
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Start, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu,
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Hinchey, Brenda S.
Huang, Shihshieh
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Ahrens, Jeffrey
Ball, James A.
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Vidya, K.R.
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Deikman, Jill
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29.5%; Score 792; DB 6; 1 larity 33.0%; Pred. No. 5.1e-68; Conservative 121; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uethy, Michael M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bin
                                                                                                                                                                                                                                                                                                                                                                     Zhanguo
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Matches

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APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SED ID NO 59005

LENGTH: 515

TYPE: par-
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ORGANISM: Zea mays
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101 SAVFRSHLFGSATVVTSDAEVSRFVLHSDARAFVPWYPRSLTELMGESSILLINGSLQRR
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                                                                                                                                                   Similarity
                             K-IYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGDMHRD 135
                                                                                  LFLILLKRR------NRKTRFULPPGKSGWPFLGETIGYLKPYTATTLGDFMQQHVSKYG
                                                                 LWYLLSRRRAAGGSKDKERAARLPPGSFGWPLVGETLDFVSCAYSSRPEAFVDKRRLLHG
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                                                                                                                               29.5%; Score 790; DB 6; I
33.4%; Pred. No. 7.9e-68;
tive 119; Mismatches 170;
                                                                                                                                                               Length 515;
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Maximum DB :
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Maximum Match 100%
Listing first 45 summaries
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               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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2681
1 MFETEHHTLLPLLL
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2: pir2:*
3: pir3:*
4: pir4:*
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            MFETEHHTLLPLLLLPSLLS.....FAFPFVDFPNGLPIRVSRIL 513
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284	287	287.5	288.5	90.5	91.5	91.5	292	294	294	94.5	297	297	99.5	
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cytochrome P450 ho	cytochrome P450 3A	cytochrome P450 [i hypothetical prote	cytochrome P450, g	cytochrome P450 mo	lanosterol 14alpha	cytochrome P450 2B	cytochrome P450 2B	flavonoid 3',5'-hy	probable Cytochrom	cytochrome P450 2B	cytochrome P450 2A	testosterone 16alp	cytochrome P450 2B	

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A; Reference number: S55379
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A; Molecule type: mRNA
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R;Szekeres; M.; Nemeth, K.; Koncz, Z.; Nagy, F.; Koncz,
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                                                                                                                                       QQNNGASSSGSGSFSTWGNN-YMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAED
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79; Mismatches 171;
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Chin, C.W.; Chung, M.F.; Hujhes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, A;Authors: Hui, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. A;Authors: Salzberg, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Roney, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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C:Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450
C:Keywords: heme; iron; metalloprotein
C:Keywords site: heme iron (Cys) (axial ligand) #status predicted
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A; Residues: 1-512 <STO>
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C;Species: Arabidopsis thallana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Apr-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLLLPSLLSLLLFLIL-----LKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGD
                                                                                                                                                                     GCFVVPFLSAVHLDESYYKESLSFNPWRWLDPETQQKRNWRTSP
                                                                                                                                                                                                                                                                                                                                                                                                      AGNGVLGRILLEEESLPNESMADFIINLLFAGNETTSKTMLFAVYFLTHCPKAMTQLLEEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLPGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQR
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                                                                                                         GGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPNGLPIRVSR
                                                                                                                                                                                                                           GWKYLPYISAYHLDNSRYDQPNLFNPWRW-----QQQNNGASSSGSGSFSTWGNNYMPFG
                                                                                                                                                                                                                                                                                                                                             LEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPS
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76;

Gaps

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286

281

249 221 190 161 130 101 70

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346

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RESULT 5

746613
hypothetical protein F18022.190 - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C; Date: 30-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C; Accession: T48613
R; Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; submitted to the Protein Sequence Database, April 2000
A; Reference number: Z24493
A; Accession: T48613
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A;Recession: D85429
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-457 <STO>
A;Cross-references: GB:NC_001268; NID:g7270586; PIDN:CAB80304.1; GSPDB:GN00140
C;Genetics:
A;Gene: A74936380
A;Map position: 4
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
C;Reywords: heme; iron; metalloprotein
F;396/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytochrome P450 like protein [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Apr-2001 C;Accession: D85429 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999
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179; Conserv
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36.8%; Pred. No. 3.3e-48;
tive 93; Mismatches 160;
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C;Accession: T07859
R;Bishop, G.J.; Harrison, K.; Jones, J.D.
Plant Cell 8, 959-969, 1996
A;Title: The tomato Dwarf gene isolated by heterologous A;Reference number: Z16181; MUID:96266705; PMID:8672892
A;Accession: T07859
                                                                                                                                                                                                                                                                                                                                     cytochrome P450 homolog - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999
                                                                   C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome F;273-436/Domain: cytochrome P450 homology <P45>
                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-464 <BIS>
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                                                                                                            A;Gene: dwarf
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A;Experimental source: strain GCR758
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A; Introns: 31/2; 1
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A;Molecule type: DNA
A;Residues: 1-382 <BEV'>
A;Cross-references: EMBL:DB
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 al Similarity
170; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GELGKLQIAFFLHHLVLSYRWKIKSDEMPIAHPYVEFKRGMLLEI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPNGLPIRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VFPIFTAVHLDPSLHENPFEFNPMRWTKTT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGYTNAIKVRSNRNIHQNAIIEDMNNAIREEDFLDSIISNED----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKSWKNCREVEFHKEVKIFTLSVMVNQLLSIKPEDPARLYVLQDFLSYMKGFISLPIPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKLFTSDYPKAMHDILGKYSLLLATGEIHRKLKNVIISFINLTKSKPDFLHCAENLSISI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRLFECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GWPFIGETISFFKPHRSDSIGTFLQQRVSRYGKVFKSNICGGKAVVSCDQELNMFILQNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GWPFLGETIGYLKPYTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLLGWYLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEI 344
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139/3; 204/1; 224/3; 253/3; 280/1; 315/3; 349/2
                28.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.4%;
 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87; Mismatches
Score 761.5; DB 2;
Pred. No. 7.9e-42;
0; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 815; DB 2;
Pred. No. 2.1e-45;
                                                                                                                                                                                                                                                                                                                                         #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 382;
 Indels
                                 Length 464;
                                                                                                                                                                                                                                                                     transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---AFGGGVRVCPG
61;
                                                                                       P450
                                                                                                                                                                                                                                                                    tagging encodes
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                      homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
10;
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LLLLPSLLSLLLFLILLKRRN--RKTRFNLPPGKSGWPFLGETIGYLKPYTATTLG-DFM 68

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A; Map position: 4
A; Introns: 67/2; 173/
A; Note: T18B16.200; T
C; Superfamily: Synech
C; Keywords: chromopro
F; 272-433/Domain: cyt
                                                                                                                                                                                                                                                                                                                                                                                                            cytochrome P450 - Arabidopsis thaliana
WALTERNATE names: protein T18B16.200; protein T5K18.10
N;Contains: oxidoreductase [EC 1.-.-]
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 28-Jul-2000
C;Accession: T04444; T05806
C;Becession: T04444; T05806
C;Becession: T04444; T05806
A;Reference number: Z15359
A;Accession: T04444
                                                                                                                                                                                                            A; ACCression Library DNA
A; Molecule type: DNA
A; Residues: 131-457 <BEW>
A; Cross-references: EMBL: AL022580
A; Cross-references: cultivar Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
Š
                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AL021687
A;Experimental source: cultivar Columbia; BAC clone T18B16
R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.;
submitted to the Protein Sequence Database, April 1998
                                                                                                                                                                                                                                                                                 A; Reference number: Z15453
A; Accession: T05806
                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-457 <BEV>
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                                                                                                ;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology;Keywords: chromoprotein; electron transfer; heme; iron; monooxygenase; oxido;;272-433/Domain: cytochrome P450 homology <P45>
                                                                                                                                                                                                     Genetics:
                                                   Local
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                                                 Similarity
LLLPSILSLILFLILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KFNWELAEDDQPFAFPFVDFPNGLPIRVS 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQ : | | | : | | | | | | | | : | : | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKHIMSMDPGEEET----EQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYRWEEIGGDKLMKFPRVEAPNGLRIRVS 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHS----NLSTEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGSAHKYMRGALLSLISPTMIRDQLLPKIDEFMRSHLTNW-DNKVIDIQEKTNKMAFLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNQRARYGSFFKSHILGCPTIVSMDSELNRYILVNEAKGLVPGYPQSMIDILGKCNIAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVL 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSMRFTRAVILETSRLATIVNGVLRKTTQDMEINGYIIPKGWRIYVYTRELNYDPRLYPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDLITTILYSGYETVSTTSMMAVKYLHDHPKVLEELRKEHMAIREKKKP--EDPIDYNDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IEERR------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVL
                                                                                                                                              173/3; 302/3; 358/1; 393/3
00; T5K18.10
                                                                                               cytochrome P450 homology <P45>
                                                 23.6%;
                                               Score 632; DB 2;
Pred. No. 1.8e-33;
                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -LEHQNSFLVFGGGTRQCPGKELGVAEISTFLHYFVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ASKEIQHDMLGYLMNEEATRFKLTDDEM
                                                                                                                                                                                                               BAC clone
                                                             Length
                                Indels
                                                                                                              monooxygenase; oxidoreductase
                                                                                                                                                                                                                                                                                                                               Robben,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bancroft, I.;
                                56;
                                                                                                                                                                                                                                                                                                                             J.; Volckaert,
                                Gaps
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                                                                                                                          LFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKYGKIYRSNLEGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGDM 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKF 483
                                                                                                                                                                                              IFAARDTTASVMSWILKYLAENPNVLEAVTEEQMAI-RKDKEEGES-LTWGDTKKMPLTS
                                                                                                                                                                                                                                                                                                                                                                                                 F----GKDEVLYREDLKRCYYILEKGYNSMPVNLPGTLFHKSMKARKELSQILARILSER
                                                                                                                                                                                                                                                                                                                                                                                                                                             MSMDPGEEET - - - EQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEER
                                                                                                RVIQETLRVASILSFTFREAVEDVEYEGYLIPKGWKVLPLFRNIHHSADIFSNPGKFDPS
                                                                                                                                                                                                                                                                                                                                             KLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLG-WVLKHSNLSTEQILDLILSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAKLRKLVLRAFMPESIRN-MVPDIESIAQDSLRSW-EGTMINTYQEMKTYTFNVALLSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKHI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRYGSVFKTHVLGCPCVMISSPEAAKFVLVTKSHLFKPTFPASKERMLGKQAIFFHQGDY
-VAPKPNTFMPFGNGTHSCPGNELAKLEMSIMIHHLTTKY
                                                                                                                                                                                                                                                                                                 -QNGSSH-----NDLLGSFMGDKEELTDEQIADNIIGV
                                                                                                                                               428
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                                                                                                                                                                                                                                                                                                 272
                                                                                                                                                                                                                                                                                                                                                308
                                                                                                                                                                                                                                                                                                                                                                                                                                                249
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probable cytochrome P450 At2g29090 [imported] - Arabidopsis thaliana N;Alternate names: cytochrome P450 homolog T914.17 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001 C;Accession: T02739; D84692 R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, submitted to the EMBL Data Library, August 1998 A;Description: Arabidopsis thaliana chromosome II BAC T914 genomic sequence. A;Reference number: Z14710 A;Reference number: Z14710

A; Molecule type: DNA A; Residues: 1-482 < ROU> A; Status: translated from GB/EMBL/DDBJ

A; Cross-references: EMBL: AC005315; NID: g3461834; PID: g3461849

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ve Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84692 A; Experimental source: cultivar Columbia
R; Lin, X.; Kaul, S.; Kounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.
M.; KOO, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, (C.D.; Fujii, .Y ayam, L.; Tallan, Ven=er

A; Status: preliminary

A; Molecule type: DNA A; Residues: 1-482 <STO> A; Cross-references: GB:AE002093; NID:g3461849; PIDN:AAC33235.1; GSPDB:GN00139

A; Gene: At2g29090; T9I4.17

A:Map position: 2
A:Introns: 80/2; 187/3; 238/3; 321/3; 351/3; 413/3; 453/2
C:Superfamily: Synechocystis cytochrome P450 slr0574; cyto
F;291-453/Domain: cytochrome P450 homology <P45> cytochrome P450 homology

Matches Query Match Best Local Similarity Conservative 22.8%; 29.8%; 101; Score 611; DB 2; Pred. No. 4.5e-32; Mismatches Length 482 Indels 68; Gaps

16 PSLLSLLLFLILLK----- RRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQ 69

Ñ

TOO F NEMANHI MSMUPGEEETEQLKKE	-	
185	Qy 77KIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILG 121	
7 125 MLVLVGDMHRDMRSISLNFLSHARLR :: : : : 132 IMAKOGEKHRVLRGIVANSISVIGLE	ω	
Y 65 GDFWQQHVSKYGKIYRSNLFGEPTIV :::: 72 EDFVNPRIIKHGNIFKTRIMGSPTIV	Best Local Similarity 27.3%; Score 581; DB 1; Length 487; Best Local Similarity 27.3%; Pred. No. 4e-30; Matches 143; Conservative 100; Mismatches 205; Indels 76; Gaps 11; Db	
Y 12 LLLLPSLLSLLLFLILLKRR : : : : : LCIAATISSTLFFFRKKHHRFITKKI	romoprotein; heme; iron;	
Query Match 21.6%; Score Best Local Similarity 28.8%; Pred. Matches 147; Conservative 107; Mis	tics: 13695c position: 4COP9-4G3845 rfamily: Synophocyetis cytooboomo n/E0 classes.	
C;Superfamily: Synechocystis cytochrome C;Keywords: heme; iron; metalloprotein F;432/Binding site: heme iron (Cys) (axi	ence not shown; translation not shown	
C;Genetics: A;Gene: At2g42850 A;Map position: 2	is of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal ber: A71400; MUID:98121113; PMID:9461215 1417	
A; Residues: 1-485 <sto> A; Cross-references: GB: AE002093; NID:q4</sto>	; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomeneches, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans	•
numb : A84 relim	NVE, K.; GOOdman, H.; Dean, C.; Bergkamp, R.; Dirk R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel htian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.	
iss, p.; Nierman, W.C.; White, O.; Eistature 402, 761-768, 1999 Fitle: Sequence and analysis of them:	nce_revision 10-Sep-1999 #text_change 16-Jun-2000	
; Lin, X.; Kaul, S.; Rounsley, S.D.; SI	es: Arabidopsis thaliana (mouse ear cress)	
probable cytochrome P450 [imported] - Ar C;Species: Arabidopsis thaliana (mouse-c;Date: 02-Feb-2001 #sequence_revision C;Accession: A84859	e P450 d13695c - Arabidopsis thaliana s: oxidoreductase (EC 1)	
RESULT 10	449 TISEKWEVIGDEEGIQYGPFPVFKKGLPIRVTPI 482	
Db 438 FAKMQMAVFIHHL-FRYRWSMKSGT	VLKFNWELAEDDOPFAF-PFVDFPNGLPIRVSRI 512	
Qy 467 LAKLEMAVFIHHLVLKFNWELAÉDD	448	
Db 388 G-YPHIHFNSEKYEDPYAFNPWRWE	479	
Qy 407 PVISAVHLDNSRYDQPNLFNPWRWQ	401	
QY 347 AKKELGESELNWDDYKKMDFTQCVI		
	301 ILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEI-ARAKKELGESELNWD 359	
QY 287 LGWVLKHSNLSTEQILDLILSLLFA	AKDQKRNGLSDSQ 283	
Db 231 EADISWQARKRMMKLLRKTVLTKRA	RKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQ 300	
Qy 233QSRATILKFIERKMEERKL	250	
Db 173 KILIGCLAKKVMGEMEPEAAKEL	245	
Qy 182 KFTFNLMAKHIM-SMDPGEEETEQL	193	
Db 113 ENNLFLQSKESHKHVRNLTFQLLGF	188	
Oy 122 KWSMLVLVGDMHRDMRSISLNFLSH	135	
Db 63 ADESSIHLSFERTSLEGDKAIISME	138	
	Db 20 PALITLTIVVVVVVLLFKWWLHWKEORLRLppggwgt.pvTgemtptvmenn-wgenn 75	

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e P450 slr0574; cytochrome P450 homology
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ismatches 203; Indels 53; Gaps
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--ear cress)
- 02-Feb-2001 #text_change 23-Mar-2001
EYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFI 242
                                        ESLIPKLCDTVKFHHETEWRGKEEISLYRSAKVLT 191
                                                                                   RTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFT 184
                                                                                                                                                                                                            RRNRKTRENLPPGKSGWPELGETIGYLKDYTAT-TL 64
: | | | | | | | | : | | | : | | ;
KIOKKKK--LLPGEMGLPWIGETMDFYKAQKSNRVF 71
                                                                                                                                                                                                                                                                                                                                                                                   kial ligand) #status predicted
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487; PMID:10617197
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.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
sen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
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                                                                                                                           VVNGAEANRLILSNEFSLVVSSWPSSSVQLMGMNC 131
                                                                                                                                                    VSADAGLNRFILQNEGRLFECSYPRSIGGILGKWS 124
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RESULT 11
H86185
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: H86185
C: Accession: H86185
T.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dew ansen, N.F.; Hughes, B.; Huizar, L.

A; Authors: Hunter, J.C.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.;
C.A.; Li, J.H.; Li, Y.; Lin, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Ma

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; T

Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719; PMID:11130712
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C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
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A; Residues: 1-490 <STO>
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133; Conserv
      DNLLNVK - - -
                                                                                                       FMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEM
                                                                                                                                                             TYIPYIEENVITVLDKWTKMGEFEFLTHLRKLTFRII-MYIFLSSESENVMDALEREYTA
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                                         SKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACP
                                                                                                                                                                                                                                                                                                                        ENRHYLPPGDLGWPFIGNMLSFLRAFKTSDPDSFTRTLIKRYGPKGIYKAHMFGNPSIIV
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                                                                                LNYGVRAMAVNIPGFAYHRALKARKTLVAAFQSIVTERR-----NQRKQNILSNKKDML
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  -DED-----GKTLDDEEIIDVLLMYLNAGHESSGHTIMWATVFLQEHP
                                                                                                                                                                                                                                                                                                                                                                                                                         21.6%;
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107; Mismatches
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Maiti, R.; Marziali
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A;Introns: 70/2; 178/3; 229/3; 312/3; 343/3; 346/1; 381/3
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-455 <JOR>
A;Cross-references: EMBL:AL353992; GSPDB:GN00061; ATSP:F14D17.40
A;Experimental source: cultivar Columbia; BAC clone F14D17
C;Genetics:
A;Gene: ATSP:F14D17.40
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T48973
Cytochrome P450-like protein - Arabidopsis thaliana
N;Alternate names: protein F14D17.40
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C;Accession: T48973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 TDKDVNMEILRQENKSFILSYPDGLMKPLGKDSLFLKIGNIHKHIKQITLHLLSSEGLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 NRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVS 91
                                                                                                                                                           VINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWR
  DDQPFAFPFVDFPNGLPIRVSR 511
                                                                              WQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAE
                                                                                                                                                                                                                         AGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYK-KMDFTQC
                                                                                                                                                                                                                                                                                                                                                                                                     FMKGV-----
                                                                                                                                                                                                    VTQDTTSKAICLAVKFLLENPKVLAELKKEH-EVILESREDKEGGVTWEEYRHKMTFTN-
                                                                                                                                                                                                                                                                                                                    EDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSN-----LSTEQILDLILSLLF
                                                                                                                                                                                                                                                                                                                                                               KLMGIFKAFTFDWFRTSYLISAGKGLYNTLW--ACREGMREIKDIYTMRKTSEEKY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILLKDVERHTLFYLDSWQQNSIFSAQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPKSNGKLPPGSMGFPIIGETLDFFKPYGFYEISPYLKKKMLRYGPLFRTNILGVKTVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLPFGAGSHLCPGNDLAKLEISIFLHHFLLKYQVKRSNPECPVMY 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAF 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEMNGYLIPKGWKVLTWFRDVHIDPEVFPDPRKFDPARW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRYKGYDIPSGWKYLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84;
                                                                                                                                                                                                                                                                                                                                                                                                     -VSAPLNLPGTAYHKALQSRATILK--FIERKMEERKLDIKE 255
                                         -KTFMVFGTGLRQCAGAEFARLQISVFLHHLVTTYNFSLHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 577; DB 2; Pred. No. 6.6e-30;
                                                                                                                        -- MKSGYTIPAGWIVMIIPSVVHFDPEIYENPFEFNPWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                 DDFLNTAIEESEKAGELLNENAIITLIFTLSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 455;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100;
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RESULT 14
D96813
hypothetical protein T30F21.17 [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change
C; Accession: D96813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: At2g32440
A;Map position: 2
C;Superfamily: Syn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-489 <STO>
A;Cross-references: GB:AE002093; NID:g3831452;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: B84733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shea, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable cytochrome P450 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001 C;Accession: B84733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
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                                                                                                                                     LEISIFLHHFLLKYRVERSNPGCPVMF----LPHNRPKDNCLARITRTM 488
                                                                                                                                                                      LEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPNGLP-----IRVSRIL 513
                                                                                                                                                                                                                                    SAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAK
                                                                                                                                                                                                                                                                    RAPGQKLTLKETREMYYLSQVIDETLRVITFSLTAFREAKSDVQMDGYIIPKGWKVLTWF
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                                                                                                                                                                                                                                                                                          VLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKK
                                                                                                                                                                                                                                                                                                                                                                                                       KKLVAAFQSIVTNRRNQRKQNISSNRKDMLDNLIDVKDE-----NGRVLDD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLSHLRKLTFKVI-MYIFLSSESEHVMDSLEREYTNLNYGVRAMGINLPGFAYHRALKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TMKLIGRKSFVGISFEEHKRLRRLTSAPVNGPEALSVYIQFIEETVNTDLEKWSKMGEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFKTSDPESFIQSYITRYGRTGIYKAHMFGYPCVLVTTPETCRRVLTDDD-AFHIGWPKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLLPLLLLPSILSLLLELI--LIKRRN-------RTTRENLPDGKSGWPELGETIGYLK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYTATTLGDFMQQHVSKYGK--IYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGLILMWFP-LIILGLFVLKWVLKRVNVWIYVSKLGEKKHYLPPGDLGWPVIGNMWSFLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechocystis cytochrome P450 slr0574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -ATILKFIERKMEERKLDI--KEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                     ·EEIIDLLLMYLNAGHESSGHLTMWATILMQEHPMILQKAKEEQERI--VKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.4%; Score 547.5;
27.6%; Pred. No. 5.9
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5; Mismatches 211;
                02-Mar-2001 #text_change 19-Apr-2002
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                                                                                                                                                                                                      -GYTPKAGTFLPFGLGSHLCPGNDLAK
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Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Li, Y.; Lin, S.X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Accession: D96813

A;Status, C. P. Palminson, P. P. Palminson.

A; Accession: D96813

A; Status, C. P. Palminson, P. P. Palminson.

A; Status, P. Palminson, P. P. P. Palminson, P. P. Palminson
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C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-460 <STO>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene:
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430 FSMVQDSEIIRSPFHQYTKDLLINISQ
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                                                                                                                                                   NPWRWQQQNNGASSSGSGSFSTWGN-NYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFN 484
                                                                                                                                                                                                                                               TOCVINETLARGNVVRFLHRKALKDVRYKG-YDIPSGWKVLPVISAVHLDNSRYDQPNLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                               TNMVSNEVLRLANTTPLLFRKAVQDVEIKGKY------YLEVIHMGFG------
                                                                                                                                                                                                                                                                                                                   LAFALREGTSSCTALAVKFISKDPKVLAELKREHKAIVDNRKD-KEAGVSWEEYRHNMTF 340
                                                                                                                                                                                                                                                                                                                                                                           LLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYK-KMDF 366
                                                        WELAEDDQPFAFPFVDFPNGLPIRVSR
                                                                                                                      --WLWQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEERKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                    -----EEAIQVMKDVLMMRKETREKQ---EDFLNTLLEELEKDGSFFDQGSAINLIFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKH-----SNLSTEQILDLILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {\tt HKYLQKITMQILGSEGLKQTMLGNMDKATRDHIRSIASQGSFNVRKEVENLVVAYMTPKL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | IRYGPLFRTNIFGSKTVVSTDPDVIHQIFRQENTSFELGYPDIFVKVFGKDNLFLKEVFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLLPSLLSLLLFLILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDEWQQHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MLMVALVVVRISHWLYRWSNPKCPGKLPPGSMGFPIIGETLDFFKPCGVEGIPTFVKKRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.6%;
                                                                                                    -GKEMIWGSKTFMAFGYGVRLCVGAEFSRLQMAIFLHHLVAYYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102;
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Pred. No. 9.3e-25;
02; Mismatches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NID:94836883; PIDN:AAD30586.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----LNAFNLDWFKSF-LRLSTWKAVTKALKSR---
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Maiti, R.; Marzia
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RWinkler, R.G.; Helentjaris, T.
RWinkler, R.G.; Helentjaris, T.
Plant Cell 7, 1307-1317, 1995
A:Title: The maize dwarf3 gene encodes a cy
A:Reference number: Z14648; MUID:96004534;

cytochrome P450-mediated 4; PMID:7549486

early step

in

gibbe

Accession: T02263

cytochrome P450 DWARF3 - maize
M;Contains: oxidoreductase (EC 1.-.-)
C;Species: Zea mays (maize).
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: T02263

21-Jul-2000

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A; Description: involved in an early step in gibberellin biosynthesis
A; Description: gibberellin biosynthesis
C; Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: T02263
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-519 <WIN>
A;Cross-references: EMBL:U32579; NID:g987266; PIDN:AAC49067.1; PID:g987267
A;Experimental source: strain B73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;325-488/Domain: cytochrome P450 homology <P45>
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A;Gene: dwarf3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.3%; Score 491.5; DB 1; Length 519; Best Local Similarity 28.2%; Pred. No. 2.7e-24; Matches 129; Conservative 91; Mismatches 189; Indels 49;
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                        STWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKF 483
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                                                                                  RQATRDVFVNGYLIPKGWKVQLWYRSVHMDPQVYPDPTKFDPSRWE-----GHSPRAGTF 456
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Search completed: June 10, 2003, 21:59:31 Job time: 30 secs

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CP46_MOUSE
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Q9m066 arabidopsis
Q43147 lycopersico
Q23051 arabidopsis
P79739 brachydanio
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Q95078
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4 saccharomyc
1 arabidopsic
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4 homo sapian
6 drosophila
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4 mesocricetu
2 rattus norv
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8 oryctolagus
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4 gallus gall

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	77; CAA6 88; CAA6 1237; BA1 1237; BA2 1267; p45 167; p45 100086; o ase; Mou 1 418 472 AA;	SMILARITY: BELONGS' SWISS-PROT entry is sen the Swiss Insti European Bioinformat by non-profit ins: fied and this statem fied an email to lice	ROM N.A. Columbi [71969; tani H. Tabat Tabat analys the 1.	COlumbi Columbi 200769; Nemet Redei Eeroids J cell e	8 (Rel. 37, 1 (Rel. 40, 1 (Rel 40, 1 (Pel 50, 90A1 CYP90 OR C 5 thallana Viridiplan Viridiplan yta; Magnol 1; Brassica		10.7 10.6 10.5 10.5 10.5 10.5 10.5 10.5 10.4
))	; X87367; CAA60793.1;; X87368; CAA60794.1;; X87368; CAA60794.1;; AB005237; BAB09663.1; arPro; IPR001128; Cytochr i; P\$00067; p450; 1. SITE; P\$00086; CYTOCHROME JORG ductase; Monooxygenas ZMEM 1 21 21 21 31MG 4.18 4.18 4.18 4.18 4.18 4.18 4.18 4.18	SIMILARITY: BELONGS TO THE CYTOCHR SWISS-PROT entry is copyright. It ween the Swiss Institute of Bioinf European Bioinformatics Institute. by non-profit institutions as I lified and this statement is not rem titles requires a license agreement send an email to license@isb-sib.ch	ia; PubMed=93; PubMed=93; ., Nakamura ta S.; sis of Arak sis of Arak .6 Mb regic	a; pubMed= h K., K G.P., W rescue longati	37, Crea 37, Last 40, Last DA1 (EC 1 ROPD of ana (Mouse plantae; ; plantae; ; proliophy;	STANDARD;	533 502 502 503 504 504 504 503 513
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Query Match Best Local Similarity

36.5%; 41.9%;

Score 978.5; DB 1; Pred. No. 1.7e-51;

Length 472

Matches

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RESULT
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                       Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T. Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
                                                                              Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G., Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N., Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Welchselgartner M., de Simone V., Obermaler B., Mache R., Muelle Kreis M., Delseny M., Pulgdomenech P., Watson M., Schmidtheini T
                                                                                                                                                                                                                                                                                                                                   Kim G-T., Tsukaya H., Uchimiya H.;
"The ROTUNDIFOLIA3 gene of Arabidopsis
of the cytochrome P-450 family that is
polar elongation of leaf cells.";
Genes Dev. 12:2381-2391(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytochrome P450 90C1 (EC 1.14.-.-) (ROTUNDIFOLIA3).
ROT3 OR CYP90C1 OR AT4G36380 OR C7A10.980 OR F23E13.220
                                                                                                                                                                                                                     STRAIN=cv. Columbia;
MEDLINE=20083488; PubMed=10617198;
Langham
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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McCullagh B.,
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Bilham
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Robben
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                                                                                                        Mueller M.,
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δõ

Matches

Similarity

Conservative

96; Pred.

Mismatches

Indels

78;

Gaps

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----LKRRNRKTRFN---

LPPGKSGWPFLGETIGYL---

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RA Bernelser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert D., Herzl A.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Villaler P., Herzl A.,
RA Neumann S., Argiriou A., Villale D., Liguori R., Piravandi E.,
RA Neumann S., Argiriou A., Villale D., Liguori R., Piravandi E.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Cibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hiller L.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonoiu B., Scholler M., Hose M., Hose M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McComble W.R.;
Thallana. ".
The Scholar M., Martienssen R., McComble W.R.;
Thallana.".
      Query Match
Best Local
                                                                                                                                                                                                                                                        EMBL; AB008097; BAA37167.1; --
EMBL; AL161589; CAB80304.1; ALT_INIT.
EMBL; Z99708; CAB16850.1; ALT_INIT.
EMBL; AL022141; CAA18139.1; ALT_SEQ.
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
Oxidoreductase; Monooxygenase; Transmembrane; Helegalonia (Control Control Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -I- FUNCTION: MIGHT BE INVOLVED IN THE BIOSYNTHESIS OF IMPORTANT FOR THE POLAR ELONGATION OF CELLS DURING -I- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic 1
                                                                                                                                                                                                        TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Van der Schueren J., Grymonprez B.,
Braeken M., Weltjens I., Voet M., Bu
Weitzenegger T., Bothe G., Ramsperg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 402:769-777(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: UBIQUITOUS.
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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                                                                                                      524 AA;
                                                                                                                                                                                                                             reticulum; Multigene family.
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                                                                                                         59389
   32.2%;
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F -> L (IN REF. 2).
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                                                                                                                                                                                                        POTENTIAL
3 864;
1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                     BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage by
                                  Length
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Cytochrome P450 85 (EC 1.14.-.-) (Dwarf protein).
                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                 Bishop G.J., Harrison K., Jones J.J.G.D.;
"The tomato Dwarf gene isolated by heterologous transposon encodes the first member of a new cytochrome P450 family.", Plant Cell 8:559-969(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CV. GCR758;
MEDLINE=96266705; PubMed=8672892;
               PROSITE; PS00086; CYTOCHROME_P450;
                                           Pfam; PF00067; p. PRINTS; PR00385;
                                                              InterPro; IPR001128; Pfam; PF00067; p450;
                                                                                                               EMBL; U54770; AAB17070.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lycopersicon esculentum (Tomato)
                                                                                                                                                                                                                                                                                                                                                             - SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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MEDLINE-21016719; PubMed-11130712;
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
Theologis A., Bicker J.R., Palm C.J., Bowman C.L., Brooks S.Y.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Dunn P., Etdu P., Feldblyum T.V., Feng J.-D., Fong B., Huizar L.
Dunn P., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.
Hunter J.L., Jenkins J., Johnson Hopson C., Khan S., Khaykin E.,
Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Cytochrome P450 88A3 (EC 1.14.-.).
CYP88A3 OR ATIGO5160 OR YUP8H12.23.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideursids II; Brassicales; Brassicaceae; Arabidopsis.
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BINDLNG 414 414 HEME (BY SIMILARITY).
SEQUENCE 464 AA; 53706 MW; D2B2lAAAB7B14E94 CRC64;
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                               Columbia;
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0; Mismatches
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Pred. No. 1.4
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                                                                                                                                                                                                                                                                                                                                                                                                   core eudicots; Rosidae;
                                                                                                                                              Creasy T.H., Dewar K.,
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301 266 361 245

4-hydroxylase).

acid-metabolizing

Vertebrata; Euteleostomi;
Ostariophysi; Cypriniformes;

all-trans-retinoic

HYDROXYLATION. FORMS OF RA, ITS

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Bonasoro J.,

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Best Local
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15-DEC-1998
                                    CP26_BRARE P79739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M. Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.; "Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 408:816-820(2000).
-1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; Monooxygenase; Transmembrane; Heme TRANSMEM 6 26 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001128; Cytochrome_P450 Pfam; PF00067; P450; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                        FLPFGAGSHLCPGNDLAKLEISIFLHHFLLKYQVKRSNPECPVMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTSDTCRRVLTDDD-AFKPGWPTSTMELIGRKSFVGISFEEHKRLRRLTAAPVNGHEALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQHVSKYGK--IYRSNLFGEPTIVS
                                                                                                                                                                          YMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAF
                                                                                                                                                                                                           VEMNGYLIPKGWKVLTWFRDVHIDPEVFPDPRKFDPARW---DNG----
                                                                                                                                                                                                                                          VRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNN
                                                                                                                                                                                                                                                                                EVLQRAKAEQEMILKSRPE-GQKGLSLKETRKMEFLSQVVDETLRVITFSLTAFREAKTD
                                                                                                                                                                                                                                                                                                               KAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKD
                                                                                                                                                                                                                                                                                                                                                 DNLLNVK----DED-----GKTLDDEEIIDVLLMYLNAGHESSGHTIMWATVFLQEHP
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439
490 AA;
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                                                    STANDARD;
 37,
37,
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 Created)
Last sequ
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Best Local S
Matches 144
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PROSITE; PS00086; CYTOCHROME_P450; 1.

Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome; Endoplasmic reticulum.

BINDING 438 438 HEME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 271:29922-29927(1996).

-I- FUNCTION: PLAYS A KEY ROLE IN RETINOIC ACID METABOLISM.

-RETINOIDS, INCLUDING ALL-TRANS-RETINOIC ACID (RA) AND IT

STEREOISOMER 9-CIS-RA. CAPABLE OF 4-HYDROXYLATION; HYDRO

RESPONSIBLE FOR GENERATION OF SEVERAL HYDROXYLATED FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WHILLINE-97094702; PubMed-8939936; White J.A., Guo Y.-D., Baetz K., Beckett-Jones B., Hsu K.E., Dilworth F.J., Jones G., Petkovich M.; "Identification of the retinoic acid-inducible all acid 4-hydroxylase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U68234; AAC60045.1; -
ZFIN; ZDB-GENE-990415-44; cyp26.
InterPro; lFR001128; Cytochrome_P450.
Pfam; PF00067; P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Verto
Actinopterygii; Neopterygii; Teleostei; Ostan
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Last annotation update) Cytochrome P450 26 (EC 1.14...) (Retinoic acceptochrome) (P450RAI) (Retinoic acid 4-hydrox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDUCTION: BY RETINOIC ACID.
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INCLUDING 4-OH-RA AND 4-OXO-RA.
SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
                                                                                                                                                        173
                                                                                                                                                                                           173
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                                                                                                                                                                                                                                                                                                                                                                                                                                     144;
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                                                                                                                    ALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWV
                                                                                                                                                                                                                                              ILGKWSMLVLVGDMHRD-----MRSISLNFLSHARLRTILLKDVERHTLFVLDSW-QQNS
                                                                                                                                                                                                                                                                                               ---LQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRT
                                                                                                                                                                                                                                                                                                                                                                  YTLMVTFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQLI--
                                                                                                                                                                                                                                                                                                                                                                                                    HTLLPLLLLPSLLSLLLFL-----ILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKP
                                                 LKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKE
                                                                                   GLRAR----NFIHSKIEENIRKKIQDDDNENEQKYKDALQLL----IENSRRSDE-----
                                                                                                                                                        CVLVYPEMKKLMFRIAMRILLGFEPEQIKTDEQELVEAFEEMIKNLFSLPIDVPFSGLYR
                                                                                                                                                                                                                          ILGSDTLSNVHGVQHKNKKKAIMRAFSRDALEH----YIPVIQQEVKSAIQEWLQKDS
                                                                                                                                                                                                                                                                                                                             YTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGG
                  ----PFSLQAMKEAATELLFGGHETTASTATSLVMFLGLNTEVVQKVREE-----VQEKVE
                                                                                                                                                                                         IFSAQDEAKKFTFNLMAKHIMSMDPGEEET--EQLKKEYVTFMKGVVSAPLNLPGTAYHK
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Pred. No.
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Mismatches

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.8e-DB 1;

> Length 492 CRC64;

Indels

66;

Gaps

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118

61

230 172 172

290 232

sequence

update

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Best Local
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15-JUN-2002 (Rel. 41, Last annotation update)
Cytochrome P450 88A1 (EC 1.14.---) (DWARF3 protein).
CYP88A1 OR D3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in Gibberellin biosynthesis."; Plant Cell 7:1307-1317(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. B73;
MEDLINE=96004534; PubMed=7549486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Str. Spermatophyta; Magnoliophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00067; p450;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: Gibberellin biosynthesis; early step.
TISSUE SPECIFICITY: EXPRESSED IN ROOTS, DEVELOPING
VEGETATIVE MERISTEM, AND SUSPENSION CULTURE CELLS.
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
           187
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                                                          LLKDVERHTLFVLDSW-QQNSIFSAQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVT
                                                                                                                 AEGCKQVLMDDDA--FVTGWPKATVALVGPRSFVAMPYDEHRRIRKLTAAPINGFDALTG
                                                                                                                                                                      DAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTI 152
                                                                                                                                                                                                                              RARLPPGEMGWPLVGGMWAFLRAFKSGKPDAFIASFVRRFGRTGVYRSFMFSSPTVLVTT
                                                                                                                                                                                                                                                                               RENLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQHVSKYGK--IYRSNLFGEPTI-VSA
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57906 MW; 0F8977A024316D95 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                 18.3%;
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                                                                                                                                                                                                                                                                                                                                             91;
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                                                                                                                                                                                                                                                                                                                                          Score 491.5; DB Pred. No. 2e-22; 1; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    naneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamur. Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Oki Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasu Tabata S.;
                             Complete proteome. BINDING 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome."; DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative cytochrome P450 120 (EC 1.14.-.+):
                                                                         PROSTEE; PSUUU86; CYTOCHROME_P450; 1.
Hypothetical protein; Oxidoreductase;
                                                                                                            Pfam; PF00067; p450; 1
PROSITE; PS00086; CYTC
                                                                                                                                                                                                EMBL; D64003; BAA10496.1;
                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entire genome and assignment of potential protein-coding DNA Res. 3:109-136(1996).
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                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                             non-profit institutions as long and this statement is not removed.
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                                                                                                                                                                IPR001128; Cytochrome_P450
  444 AA;
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     MW:
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                                HEME (BY SIMILARITY)
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8F62A9EED3B54BDC
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                                                                                 Monooxygenase; Heme;
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Miyajima

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Nakamura Y.,

Yasuda Okumura

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                                                                                                                                                                                                    Fujii H., Sacc
Fujii H., Sacc
Financiiva
                                                                                                                                                                                                                                                                                                                                        GP26_MOUSE STANDARD; PRT; 497 AA.
055127; Q9R1F4;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytochrome P450 26 (EC 1.14.--) (Retinoic acid-metabolizing cytochrome) (P450RAI) (Retinoic acid 4-hydroxylase).
CYP26A1 OR CYP26 OR P450RA.
                                                   acid metabolism in F9 cells are regulated by gamma and retinoid X receptor alpha.";
J. Biol. Chem. 273:2409-2415(1998).
                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
    MEDLINE-20515038;
                                                                                                                                                                                  Kato S., Hamada H.; "Metabolic inactivation of retinoic acid by a novel P450 differentially expressed in developing mouse embryos.";
                                                                                       Abu-Abed S.S., Beckett B.R., Chiba H., Chithalen J.V., Jones G., Metzger D., Chambon P., Petkovich M.; Mouse P450RAI (CYP26) expression and retinoic acid-inducible retinoic mouse P450RAI (CYP26) expression and retinoic acid-inducible retinoic
                                                                                                                                                                                                                          MEDLINE-97392446; PubMed-9250660;
Fujii H., Sato T., Kaneko S., Gotoh O.,
                            SEQUENCE FROM N.A.
                                                                                                                                MEDLINE-98113212; PubMed-9442090;
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                          J. 16:4163-4173(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKHIMSMDPGEE--ETEQLKKEYVTFM 213
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    PubMed=11063033;
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29.7%;
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Pred. No. 8.
                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .5e-22;
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                                                                               retinoic acid
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                                                                               receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00086;
                                                                                                                                 177
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                                                                                                                                                          AQDEAKKFTFNLMAKHIMSMDPGE----EETEQLKKEYVTFMKGVVSAPLNLPGTAYHKA
                                                                                                                                                                                   TILGAGCLSNLHDSSHKQRKKVIMQAFSREALQCYVLV-IAEEVSSCLEQWLSCGERGLL
                                                                                                                                                                                                           GILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQ--NSIFS
                                                                                                                                                                                                                                                              PYTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIG
AKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVL
                                                                             VKARNLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWE
                                                                                                                                VYPEVKRLMFRIAMRILLGCEPGPAGGGEDEQQLVEAFEEMTRNLFSLPIDVPFSGLYRG
                                                                                                                                                                                                                                                                                          LPALLASALCTFVLPLLLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETL----
                                                 LGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIAR
                                                                                                      LQSRATILKFIERKMEE---RKLDIKEED----QEEEEVKTEDEAEMSKSDHVRKQRTDDDL
                                                                                                                                                                                                                                      -QMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVHWPASVR
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use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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InterPro; IPR001128; Cytoc
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                EMBL; Y12657; CAA73206.1; -. EMBL; AF115769; AA017217.1; -. EMBL; BC012673; AAH12673.1; -. HSSP; P14779; 1JPZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paine C.T., Paine M.L., Snead M.L.;
"Identification of tuftelin" and amelogenin-interacting proteins using the yeast two-hybrid system.";
Connect. Tissue Res. 38:257-267(1998).
                                                                                                                                                                                                                                        Oxidoreductase; Monooxygenase;
10 LPLLLLPSL----LSLLLFLILLK-----RNRKTRFNLPPGKSGWPFLGETIGYLK
                                    Conservative
                                                                                                                                                                                                                                                              CYTOCHROME_P450;
                                                     17.2%;
28.4%;
                                                                                                             56177 MW;
                                                                                                                                                                                                                                                                                                                  Cytochrome_P450
                              78;
                                                                                                                             S -> T (IN REF.
L -> P (IN REF.
I -> T (IN REF.
Y -> H (IN REF.
                                                       Pred.
                                                                     Score 461;
                                                                                                                                                                                                    HEME (POTENTIAL)
                                                                                                             33B07D7C29134471 CRC64;
                                                                                                                                                                                                                                          Membrane; Heme;
                                    Mismatches
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                                                     1.2e-20
                                                                                                                                              REF.
                                                                                                                                                               REF.
                                                                       DB 1;
                                                                                                                                                                                                                                          Microsome;
                                                                     Length 497;
                                    Indels
                                    64;
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                                    Gaps
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RESULT 9
CZ6A_HUMAN
ID CZ6A_HI
AC Q9NR63
DT 15-JUN
DT 15
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           SEQUENCE
                                                                                             InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 2.
PRINTS; PR00385; p450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
Oxidoreductase; Monooxygenase; Membrane; Heme;
                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
-!- TISSUE SPECIFICITY: Highly expressed in brain, particularly in cerebellum and pons.
-!- INDUCTION: By retinoic acids (RA).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bourne S., Bauer C., Pape K., Jones T.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: Plays a key role in retinoic acid metabolism.
in the specific inactivation of all-trans-RA. Responsibl generation of several hydroxylated forms of RA, includin 4-oxo-RA, and 18-OH-RA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE-20300913; PubMed=10823918; MEDINE-20300913; PubMed=10823918; White J.A., Ramshaw H., Taimi M., Stangle W., Zhang Creighton S., Tam S.-P., Jones G., Petkovich M.; "Identification of the human cytochrome P450, P450RA predominantly expressed in the adult cerebellum and all-trans-retinoic acid metabolism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C26A_HUMAN
Q9NR63; Q9N
                                                                                                                                                                                                                                                                      EMBL; AF252297; AAF76003.1; EMBL; AC007002; AAF65576.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9NR63; Q9NP41;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytochrome P450 26A2 (EC 1.14.-.-) (P450RAI-2) (Retinoic-acid metabolizing cytochrome).
                                                                BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                       Indoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYP26A2 OR P450RAI2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENZYME REGULATION: Has a preferred activity towards the following substrates: all-trans-RA > 9-cis-RA > 13-cis-RA.
SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum (By
                                                                                                                                                                                                                                                       605207;
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  68
57512
  , WM
                    HEME (POTENTIAL).

Q -> QKCTLRETRVWLPQ (IN REF.
  A06D1D9944E6726F
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CRC64;
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Best Local :
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                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytochrome P450 26 (EC 1.14...) (Retinoic acid degrading enzyme CYP26) (XCYP26) (Retinoic acid converting enzyme) (RACE).
CYP261 OR CYP26.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                      -!- INDUCTION: By retinoic acid.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                          similarity).
-!- SUBCELLULAR LOCATION: Membrane-bound.
                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-99077803; PubMed-9857192;
HOllemann T., Chen Y., Grunz H., Pieler T.;
Regionalized metabolic activity establishes boundaries of retinoic
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eamphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                          CP26_XENLA
093323;
                                                                                                                                                                                                                                                                                                                                                                                                      XENLA
                                                                                                                        EMBO
                                                                                                                                        acid
                                                                                                                                                                                                                       NCBI_TaxID=8355;
                                                                                                                                                                                                                                    Kenopodinae;
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                                                               similarity).
                                                                                                      FUNCTION: Plays a
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signalling.";
J. 17:7361-7372(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIH
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26.9%;
                                                                                                      role in retinoic acid metabolism
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Pred. No. 9.9e-20;
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This SWISS-PROT entry is copyright. between the Swiss Institute of Bioi

ght. It is produced through Bioinformatics and the EM

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RESULT 11
CP26_CHIC
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Best Local (
                                                                                                                                                    CP26_CHICK STANDARD;
Q9pUB4; Q9pUQ2;
15-JUN-2002 (Rel. 41, Cr
15-JUN-2002 (Rel. 41, La
15-JUN-2002 (Rel. 41, La
Cytochrome P450 26 (EC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                               CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF057566; AAC25158.1; -. InterPro; IPR001128; Cytochrome_P450. Pfam; PF00067; P450; 1.
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    NCBI_TaxID=9031;
[1]
                                                          Archosauria;
                                                                                                                  CYP26A1 OR CYP26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                           KLEMAVFIHHLVLKFNWEL----AEDDQPFAFPFVDFP
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                                                          Aves; Neognathae;
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                                                                                                                                                    Last sequence update)
Last annotation update)
C 1.14.-.-) (Retinoic acid
                                                                                                                                                                                                                  Created)
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Best Local
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BINDING
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GLYRGLRAR---
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RA Martinez-Ceballos E., Burdsal C.A.;

RI Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

C: I-FUNCTION: Plays a key role in retinoic acid metabolism. Appears to be involved in the specific inactivation of all-trans-RA.

CC be involved in the specific inactivation of all-trans-RA.

CR Responsible for generation of several hydroxylated forms of RA,

CC including 4-OH-RA, 4-oxo-RA, and 18-OH-RA.

CC :- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.

CC :- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.

CC :- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.

CC :- DEVELOPMENTAL STACE: Expressed at stage 7 ints expression

CC decreases in the anterior part of the embryo. From stage 7-10 its

CC decreases in the anterior part of the embryo. From stage 7-10 its

CC expression is restricted to the dorsal folds of the neural tube

CC and to rhombomere 2. At stage 10, it is expressed in the lateral

CC disappears in the neural tube, followed by a confined expression

at stage 12 to dorsal neural tube and at stage 15 an increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro, IPRO01128; Cytochrome_P450, Pfam; PF00067; P450; 2. PRINTS; PR00388; P450, PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF199462; AAF09250.1; -. EMBL; AF185266; AAD56546.1; -.
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MEDLINE-20057772; PubMed-10588879;
Swindell E.C., Thaller C., Sockanathan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; Monooxygenase; Membrane; Heme;
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the early chick embryo.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression in the ectoderm.
INDUCTION: By retinoic acid.
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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26.3%;
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Pred. No. 2.
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I -> V (IN REF. 2).
GPI -> SPT (IN REF. 2).
; 7F28B72E75C232FB CRC64;
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RESULT 12
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Trofimova-Griffin M.E., Juchau M.R.;

"Expression of cytochrome P450RAI (CYP26) in human fetal hepatic and cephalic tissues.";

Blochem. Blophys. Res. Commun. 252:487-491(1998).

-1- FUNCTION: Plays a key role in retinoic acid metabolism. Acts on retinoids, including all-trans-retinoic acid (RA) and its stereoisomer 9-cis-RA. Capable of both 4-hydroxylation and 18-hydroxylation. Responsible for generation of several hydroxylated forms of RA, including 4-0H-RA, 4-oxo-RA, AND 18-0H-RA.

-1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.

-1- TISSUE SPECIFICITY: Highest Levels in adult liver, heart, and the strength of the heart of the hear
           the European Bioinformatics Institute. The surperson by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sonneveld E., van den Brink C.E., van der Leede B.M., Schulkes R.K., Petkovich M., van der Burg B., van der Saag P.T.; "Human retinoic acid (RA) 4-hydroxylase (CYP26) is highly specific for all-trans-RA and can be induced through RA receptors in human breast and colon carcinoma cells.", Cell Growth Differ. 9:629-637(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cytochrome P450 26 (EC 1.14.-.-) (Retinoic acid-metabolizing
cytochrome) (P450RAI) (hP450RAI) (Retinoic acid 4-hydroxylase).
CYP26A1 OR CYP26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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043174;
15-DEC-1998 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones G., Petkovich M.;
Jones G., Petkovich M.;
"cDNA cloning of human retinoic acid-metabolizing identifies a novel family of cytochromes P450.";
J. Biol. Chem. 272:18538-18541(1997).
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                                                                                                                                                                                                                                                                  pituitary gland, adrenal gland, placenta and regio INDUCTION: By retinoic acid.
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                       SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/
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YRV2_CAEEL STANDARD; PRT; 520 AA 027514.
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updat putative cytochrome P450 CYP13A5 (EC 1.14.CYP13A5 OR T10B9.2.

n update)

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CAEEL

Eukaryota; Metazoa; Nemato Rhabditidae; Peloderinae;

Nematoda; Chromadorea; Rhabditida; rinae; Caenorhabditis.

Rhabditoidea;

Marian

NCBI_TaxID=6239;

Caenorhabditis elegans.

STRAIN-Bristol N2 SEQUENCE FROM N.A.

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YRV2_CAET
ID YRV2_
AC 02751
DT 01-NC
DT 01-NC
DT 30-MA
DE PUTAT
GN CYP13
OS CAENO
OC EUKAR
OC Rhabd
OX NCBI_
RN [1]
RN SEQUE
RC STRAI
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Best Local
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Pfam; pF00067; p450; 1.
PRINTS; PR00385; p450;
PROSITE; PS00086; CYTOCHROME_P450; 1.
Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome; Endoplasmic reticulum.
BINDING 42 442 HEME (POTENTIAL).
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142; Conserv
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RESULT 14
YRVA_CAEEL
ID YRVA_C
AC Q27519
DT 01-NOV
DT 01-NOV
DT 30-MAY
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Best Local
 YRVA_CAEEL
Q27519;
Q1-NOV-1997
Q1-NOV-1997
30-MAY-2000
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InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; P450; 1.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
Hypothetical protein; Oxidoreductase; Monooxygenase; Heme.
BINDING 464 464 HEME (BY SIMILARITY).
SEQUENCE 520 AA; 59524 MM; OB7B19E25B7ADF3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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1. FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE

NONOOXYGENASSES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNREL

COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.

1. SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLRTIL-----LKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKHIMSMDPGEEE
                                                                                                                                                                  GPRICIGMRLAMMEKKMLLTHILKKYTFE
                                                                                                                                                                                                         GPRLCAGSELAKLEMAVFIHHLVLKFNWE 486
                                                                                                                                                                                                                                                                                                                                               EHLEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLH-RKALKDVRYKGYD
                                                                                                                                                                                                                                                                                                                                                                                           QLTFDEIIG
                                                                                                                                                                                                                                                                                                                                                                                                                            QRTDDDLLGWYLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLMFRNPMLPKVKGIFKDGRKLPFLVSGIFPIAGTMFREFFMRFPSIQPAFDIMSTVEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGLNRFILQNEGRLFECSYPRSIGGILG-----KWSMLVLV-GDMHRDMRSISLNFLSHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPRGFPFFGVIHEFQDYENPGLLK-----LGEWTKE----YGPIYGITEGVEKTLIVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKSGWPFLG-----ETIGYLKPYTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSAD
                                                                                                                                                                                                                                                                              IPSGWKVLPVISAVHLDNSRY-DQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGG
                                                                                                                                                                                                                                                                                                                  E-----VDRECPNPEVTFDQISKLKYMECVVKEALRMYPLASIVHNRKCMKETNVLGVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEQLKKEYVTFMKGV-----VSAPLNLPGTAYHK-----ALQSRATILKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLRKIMSTVEETVVELMRH----LDDASAKGKAVDLLDYYQEFTLDIIGRIAM-----GQTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P---EFVHEVFVKQFDNFYGRKTNPIQGDPNKNKRAHLVSAQGHRWKRLRTLSSPTFSNK
                                                                                                                                                                                                                                           IEKGTNVQVDTWTLHYDPKVWGEDANEFRPERWE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IERKMEERKLDIKE----EDQ-----
(Rel. 35, 0) (Rel. 35, 1) (Rel. 39, 1)
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                                                                          STANDARD;
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annotation
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Pred. No. 1.
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Best Local S
Matches 120
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PROSITE: PS00086; CYTOCHROME_P450; 1.

Hypothetical protein; Oxidoreductase; Monooxygenase; Heme.

BINDING 464 464 HEME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WormPep; T10B9.10; CE01655.
InterPro; IPR001128; Cytochrome_P450
Pfam; PF00067; P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z48717; CAA88609.1;
HSSP; P14779; lJPZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gardner A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                 348
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                                                                                                                                                                                                                      WVLK-HSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARA
                                                                                                                                                               KKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLH-RKALKDVRYKGYDIPSGWKVL
                                                                                                                                                                                                                                                                            DIQSILEKALNKR-LEQREADEKAGIEPSGEPQDFIDLFLDARSTVDFFEGEAEQDFAKS
                                                                                                                                                                                                                                                                                                              TILKFIERKMEERKLDIKEEDQE---EEEVKTEDEAEM----SKSDHVRKQRTDDDLLG
                                                                                                                                                                                                                                                                                                                                                                                       MSMDPGEEET - - - - EQLKKEYVTFMKG - - - - VVSAPLNLPGTAYHK - - - - - ALQSRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P---EFVHEVFVKQFDNFYGRKLTAIQGDPNKNKRVPLVAAQGHRWKRLRTLASPTFSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPRGLPFLGVIHKFTNYENPGALK-----FSEWTKKYGPVYGITEGVEKTLVISD
                                                     VDTWSLHHDPKVWGDDVNEFKPERWE:
                                                                                                                              DRECPDPEVTFDQLSKLKYLECVVKEALRLYPLASLVHNRKCLKTTNVLGMEIEAGTNIN
                                                                                                                                                                                                     EVLKVDKHLTFDEIIGQLFVFLLAGYDTTALSLSYSSYLLATHPEIQKKLQEE-----V
                                                                                                                                                                                                                                                                                                                                                   M----GQEKSLMFRNPMLDKVKTIFKEGRNNVFMISGIFPFVGIALRNIFAKFPSLQMAT
                                                                                                                                                                                                                                                                                                                                                                                                                            SLRKIMGTVEESVTELVRSLEKASAEGKTLDMLEYYQE-----FTMDIIGKMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLRTI-------LLKDVER-----HTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGLNRFILQNEGRLFECSYPRSIGGILG-----KWSMLVLVGDMHRDMRSISLNFLSHA
                                                                                        PVISAVHLDNSRY-DQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518 AA;
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                                                         SGDELFFAKG-GYLPFGMGPRICIGM
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RA MOOIJman P., Klein Lankhorst R., Rose M., Hauf J., Carter P.,
RA Bernelser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert D., Herzl A.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Schon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Schon M., Martien B., Miller N., Greco T., Kemp K.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Manter J., Filton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Manter J., Spieth J., Ryan E., Madrews S., Geisel C., Layman D.,
RA Maller N., Siehner S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kreis M., Delseny M., Pulgdomenech P., Watson M., Schmidtheini T., Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P., Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F., Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F., Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E., Weltzenegger T., Bothe G., Ransperger U., Hilbert H., Braun M., Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Ketter P.
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065790; Q9SZU3;
16-OCT-2001 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40) Last sequence up 16-OCT-2001 (Rel. 40, Last annotation Cytochrome P450 91A2 (EC 1.14--). CYP91A2 OR AT4G37430 OR F6G17.80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Columbia;
MEDLINE=20083488; PubMed=10617198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytochromes P450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mizutani M., Ward E., Ohta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98281573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37:39-52(1998)
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PubMed=9620263;
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F00067; p450; 1.
PR00385; P450.
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                                                                                                                                                L-HRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGS
                                                                                                                                                                                                                             ANLLRNPEVLEKARSE-----IDEKIGKDRLIDESDIAVLPYLONVVSETFRLFPVAPF
                                                                                                                                                                                                                                                                                                                                       LQRLLDECRRDKEGNTMVNHLISLQQQQPEYYTDVIIKGLMMSMMLAGTETSAVTLEWAM
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A -> V (IN REF. 1).
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Search completed: June 10, 2003, 21:57:52 Job time: 20 secs

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Q8W1V5	Q8VWJ5	Q8W1S9	Q8WlT1	Q8W1S6	Q9SDM6	Q8VIL0	Q9SYN2	Q9AXH9	Q9SNG3	Q9C5Y2	Q8S917	Q9ZV72	Q9LVY7	004949	Q9C5Y3	Q9LXH8	Q9SJH2	Q9SHY7	Q9FQY4	023384	Q9L169	Q9AXM6	Q8W4T9	Q8VZC2	081077	Q9LJK2	Q9LG17	Q9FI38
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RESULT 1
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Best Local Sin
Matches 513;
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Choe S., Dilkes B.P., Fujioka S., Takatsuto S., Sakurai A.,
Feldmann K.A.;
"The DWF4 gene of Arabidopsis encodes a cytochrome P450 that
multiple 22alpha-hydroxylation steps in brassinosteroid
biosynthesis.";
Plant Cell 10:231-243(1998).
1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL, AF044216; AAC05093.1;
EMBL, AF044216; AAC05093.1;
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                                                                                                                                                                                                                                                                                                                                               Interpro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 513 AA; 58867 MW; B1639BDD9A4DA6
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                              MFETEHHTLLPLLLLPSLLSLLLFLILLKRRNRKTRFNLPPGKSGWPELGETIGYLKPYT
                                                                                                                                                                            Conservative
                                                                                                                                                                       100.0%; Score 2681; DB 10; Length 513; 100.0%; Pred. No. 1.6e-184; tive 0; Mismatches 0; Indels 0;
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Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,

Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,

Cheuk R., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,

Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,

Ishida J., Jiang P.X., Jones T., Kamiya A., Kariin-Neumann G.,

Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,

Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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O9SCQ9; O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Steroid 22-alpha-hydroxylase (DWF4) (AT3g50660/T3A5_40).
T3A5_40.
                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thallana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                    Cheuk R.,
                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Bloecker H., Mewes Salanoubat M.;
      Bowser
                                                                                                                                                                                                                                                   Submitted
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                                                                                  "Arabidopsis
                                                                                                                                                                                                                                                                                  SEQUENCE
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Best Local
Matches 51
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Q9LKH7;
Q1-OCT-2000
Q1-OCT-2000
Q1-JUN-2002
   Vigna radiata.
Vigna radiata.
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta; eurosids I; Fabales; Fabaceae;
                                                               Cytochrome CYP90A2.
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"Arabidopsis ORF clones.";
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Find (MAR-2002) to the EMBL/GenBar
Find (MAR-2004) to the EMBL (MAR-2004) to the EMBL (MAR-2004) to the EMBL; AL132979; CAB62455.1; -
EMBL; AF412114; AAL06567.1; -
EMBL; AF412114; AAL06567.1; -
EMBL; AF4021414; AAL06567.1; -
EMBL; AF4001128; Cytochrome_P450.

InterPro; IPR001128; Cytochrome_P450.

PRINTS; PR00385; P450.

PROSITE; PS00086; CYTOCHROME_P450; UNKI
Heme; MONDOXYGENBASE; Oxidoreductase.

SEQUENCE 513 AA; 58867 MW; B1639BDI
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99.8%;
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No. 3e-184;
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Embryophyta; Tracheophyta;

core eudicots; Phaseoleae; V

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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence)
01-MAR-2002 (TrEMBLrel. 20, Last annotation of the control of the co
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PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1
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Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome 1 BAC T9L24 genomic sequence.";
submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AC012396; AAG30983.1;
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; P450.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry
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5; Mismatches
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smatches 173;
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                                                                                                   Arabidopsis
                                                                                                                      Embryophyta; Tracheopedons; core eudicots;
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Matches
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Q9LN73;
01-OCT-2000 (TrEMBLrel. 15, C
01-OCT-2000 (TrEMBLrel. 15, L
01-JUN-2002 (TrEMBLrel. 21, L
T12C24.27.
    SEQUENCE FROM N.A.
Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim (Chao Q., Brooks S., Buehler E., Chin C., Chiou J., Choi E., Conn L., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee Lenz C., Li J., Liu A., Llu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri / Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SIMILARITY: BELONGS TO THE CYTOCHROME P45
EMBL; AB066286; BAB62109.1; -.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00067; p450; 1.
PROSITE; PS00036; CYTOCHROME_P450; UNKNOWN_1.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
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Shimada Y.;
                                                                                                                                                                                                          Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnollophyta; eddicotyledons; core et
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "P450 gene repressed by Submitted (JUL-2001) to -1- SIMILARITY: BELONGS
                                                                                                                                                                                            NCBI_TaxID=3702
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the EMBL/GenBank/DDBJ databases.
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eudicots; Rosid
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1 B., Lee J.,
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Kudd S., 1
Submitted
[2]
                                                                                                                                                                                                                 Q9LY89;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 43.9 kDa protein.
F18022_190.
                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis
                         Bevan M., Murphy G., Ridley P., Hudson S., Bar
Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                        Q9LY89
                                                                                      SEQUENCE FROM N.A.
                                                                                                                            NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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PRT;

382

Embryophyta; Tracheophyta; dons; core eudicots; Rosid

Rosidae;

Bancroft I.,

Mewes

H. E.

databases

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InterPro: IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 2.
PRINTS; PR00085; p450.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Monooxygenase; Oxidoreductase
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NCE 478 AA; 55058 MW; F67A
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                                                                                                              FNWELAEDDQPFAFPFVDFPNGLPIRVSR 511
                                                                                                                                                                                                                 LVFNPSRWE------GSKVTNASKHFMAFGGGMRFCVGTDFTKLQMAAFLHSLVTK
                                                                                                                                                                                                                                                                           QFINETARLANIVPAIFRKALRDIKFKEFVNDTDYTTPAGWAVMVCPPAVHLNPEMYKDP
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Best Local
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                                                                                                                                                                                                        Q94IW5 PRELIMINARY; PKT; 490 MA.
Q94IW5;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up.
01-JUN-2002 (TrEMBLrel. 21, Last annotation Cytochrome P450-like protein.
                   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ c

- SIMILARITY: BELONGS TO THE CYTOCHROME P450

EMBL; AP003244; BAB56089.1; -
                                                           STRAIN-CV. NIPPONBARE; Sasaki T., Matsumoto T., Yamamoto Toryza sativa nipponbare(GA3) genclone:P0419B01.";
                                                                                                                                                    Oryza sativa (Rice).
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
               interPro;
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                             NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AL163817; CAB87779.1;
-InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; P450; 1
PROSITE; P500086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Hypothetical protein; Monooxygenase; Oxidoreductas
SEQUENCE 382 AA; 43889 MW; 1BC5685AB73B4E30 CRC64;
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Pro; IPR001128; Cytochrome_P450
PF00067; p450; 1.
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                                                                                    'ROM N....
NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                               GELGKLQIAFFLHHLVLSYRWKIKSDEMPIAHPYVEFKRGMLLEI
                                                                                                                                                                                                                                                                                                                                                                     SELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPNGLPIRV 509
                                                                                                                                                                                                                                                                                                                                                                                                               VLPVISAVHLDNSRYDQPNLENPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -RAKKGDGEL-LNWEDYQKMEFTQCVISEALRCGNIVKTVHRKATHDIKFNEYVIPKGWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKSWKNCREVEFHKEVKIFTLSVMVNQLLSIKPEDPARLYVLQDFLSYMKGFISLPIPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDSWQQNSIFSAQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRLFECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.4%; Score 815; DB 10; Length 3: 34.2%; Pred. No. 1.3e-50; tive 87; Mismatches 127; Indels
                                                                                                                                                          Streptophyta; Embryophyta; Tracheophyta; yta; Liliopsida; Poales; Poaceae;
                                                                      noto K.;
genomic DNA,
                                                                                                                                                                                                                                           update;
                                                                     chromosome 1,
                                                                                                                                                                                                                              update;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase.
                                             databases
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Q9LIC5;
Q9LIC5;
Q1-CT-2000 (TrEMBLrel. 15, Created)
Q1-CT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-UN-2002 (TrEMBLrel. 21, Last annotation update)
Q2-UN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-UN-2002 (TrEMBLrel. 15, Last sequence update)
Q2-UN-2002 (TrEMBLrel. 15, Last sequence update)
Q1-UN-2002 (TrEMBLrel. 15, Last sequence update)
Q2-UN-2002 (TrEMBLrel. 15, Last sequence update)
Q2-UN-2002 (TrEMBLrel. 15, Last sequence update)
Q3-UN-2002 (TrEMBLrel. 15, Last sequence update)
Q2-UN-2002 (TrEMBLrel. 15, Last sequence update)
Q3-UN-2002 (TrEMBLrel. 15, Last sequence update)
Q4-UN-2002 (TrEMBLrel. 21, Last annotation updat
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"Structural analysis of Ar
Sequence features of the r
TAC and BAC clones.";
DNA Res. 7:217-221(2000).
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                                                                                                                                                                                                                                                                                                              Kaneko T., Kato T.,
Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                        STRAIN=COLUMBIA;
Kaneko T., Kato
                                                                                                                                                                 MEDLINE=20363099; PubMed=10907853;
Nakamurá Y.;
                                                                                                                                                                                                                         STRAIN-COLUMBIA
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
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SEQUENCE
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Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 490 AA; 54824 MW; 9EC2853BBAFBB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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173; Conserv
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                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                        Nakamura Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 813.5; DB 10; Lengtl
Pred. No. 2.4e-50;
6; Mismatches 156; Indels
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Best Local S
Matches 163
                                                                                                                                                                                                                                                                                 Q8WOR4 PRELIMINARY; P
Q8WOR4;
Q1-MAR-2002 (TrEMBLrel. 20, Cre.
Q1-MAR-2002 (TrEMBLrel. 20, Las.
Q1-UN-2002 (TrEMBLrel. 21, Las.
Putative cytochrome P450-like p.
SB32H17.4.
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InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
             Llaca V., Young S., Kovchok Submitted (JAN-2002) to the EMBL; AF466201; AAL73972.1;
                                                                                                                                                                                                                 Sorghum bloolor (Sorghum) (Sorghum vulgare).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Sorghum.
                                                                SEQUENCE FROM N.A. STRAIN-CV. BTX623;
                                                                                                                                  STRAIN=CV. BTX623;
Park Y.-J., Ramakr
 InterPro;
                                                                                                                    Submitted
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                  NCBI_TaxID=4558;
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NCE 464 AA; 52864 MW; A65E094665E5190B
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(JAN-2002) to
 IPR001128;
 Cytochrome_P450
                                                                                                                  w.,
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Last sequence update)
Last annotation updat
ke protein.
                               S., Messing J.;
EMBL/GenBank/DDBJ
                                                                                                                  SanMiguel P., Emberton J., EMBL/GenBank/DDBJ databases
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Pred. No. 1
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Best Local S
Matches 170
STRAIN-COLUMBIA;
MEDLINE-21295570;
                                                                                                                                                                                                                                                                                                                      BR6OXI.
                               SEQUENCE FROM N.A.
                                                                                                                                  Tabata S.;
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Q9FMA5 PRELIMINARY; PRT; 465 AA. Q9FMA5; 01-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update. Cytochrome P450 (Brassinosteroid-6-oxidase).
"Structural analysis of Arabidopsis thaliana chrosequence features of the regions of 1,456,315 bp physically assigned P1 and TAC clones."; DNA Res. 5:41-54(1998).
                                                                                                STRAIN-COLUMBIA;
MEDLINE-98290546; PubMed-9628582;
Sato S., Kaneko T., Kotani H., Na
                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
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PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
SEQUENCE 481 AA; 54984 MW; 6145CFEFC0FD74FE CRC64;
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                             NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
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70; Conservative
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Pred. No. 2.9
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nes 190;
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PubMed-11402205;

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RESULT Q940V4 ID Q940V4 ID Q9 AC Q9 DT 011 DT 011 DT 011 DT 011 DE AU CC SE CC
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                                                                                                    Q940V4;
Q940V4;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
AT3930180/T20F20_6.
AT3930180/T20F20_6.
AT3930180/T20F20_6.
AT3930180/T20F20_6.
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AT3930180/T20F20_6.
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AT3930180/T20F20_6.
AT3930180/T20F20_6.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
                    SEQUENCE FROM N.A.
Cheuk R., Chen H., I
Bowser L., Carninci
                                                                                                NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                    Q940V4
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Pfam; PF00067; p450; 1.
PRINTS; PR00385; p450.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 465 AA; 53767 MW; 0C00459C9C8666D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shimada Y., Fujioka S., Miyauchi N., Kushiro M., Takatsuto S., Nomura T., Yokota T., Kamiya Y., Bishop G., Yoshida S.; "Brassinosteroid-6-oxidases from Arabidopsis and tomato catalyze Plant Physiol 126:770-779(2001).

1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY. EMBL; AB009048; BAB08653.1; EMBL; AB035868; BAB08588.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                     HHLVLKFNWELAEDDQPFAFPFVDFPNGLPIRVS 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDEEIRDQVVTILYSGYETVSTTSMMALKYLHDHPKALQELRAEHLAFRERKRQ--DEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLRELMQERR-------DSGE-----TFTDMLGYLMKKEGNRYPL
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                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                    Kim C.J.,
P., Dale
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                Koesema E.,
J.M., Golds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91; Mismatches
                                                                                                                                                                                                                                                                                            PRT;
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Pred. No.
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          ma E., Meyers M.C., Banh
Goldsmith A.D., Hayashiz
                                                                                                                                                                                                                                                                                          465
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                                                                                                                           a; Tracheophyta;
eudicots; Rosid
            Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76;
                                                                                                                           Rosidae;
            Υ.,
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Q9LH81;
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Query Match
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A Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
A Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
A Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
A Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
A Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
A Palm C.J., Quach H.L., Yanda K., Yamamura Y., Yu G., Yu S.,
A Palm C.J., Davis R.W., Theologis A., Ecker J.R.;
C "Arabidopsis ORF clones.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
C -!- SIMILARTY: BELONGS TO THE CYTOCHROME P450 FAMMILY.
EMBL; AY052655; AAK96559.1; -.
BR EMBL; AY05278; AAL36078.1; -.
BR EMBL; AY05278; AAL36078.1; -.
BR EMBL; AY051128; Cytochrome_P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 465 AA; 53814 MW; 280A2
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PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Arabidopsis cDNA clones.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
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          437
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                                          NWELAEDDQPFAFPFVDFPNGLPIRVS
                                                                                                                           LFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKF 483
                                                                                                                                                                                                                                                                                                       LILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKK 363
RWEENGEDKLMVFPRVSAPKGYHLKCS
                                                                                                                                                                              MKFTRAVIFETSRLATIVNGVLRKTTHDLELNGYLIPKGWRIYVYTREINYDTSLYEDPM
                                                                                                                                                                                                                                                                        QVVTILYSGYETVSTTSMMALKYLHDHPKALEELRREHLAIRERKRP--DEPLTLDDIKS
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                                                                                               IFNPWRWMEKSLESKS---
                                                                                                                                                                                                                      MDFTQCVINETLRIGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPN 423
                                                                                                                                                                                                                                                                                                                                                                                                              ERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSN----LSTEQILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSLLQIAETLKKPEVEEYRTEFFKLVVGTLSVPIDIPGTNYRSGVQARNNIDRLLTELMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKNQRLRYGSFFKSHILGCPTIVSMDAELNRYILMNESKGLVAGYPQSMLDILGTCNIAA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MQOHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLV 127
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                                                                                                                                                                                                                                                                                                                                                                   26.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 712; DB 10;
Pred. No. 4.3e-43;
                                                                                   -----YFLLFGGGVRLCPGKELGISEVSSFLHYFVTKY
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463
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PRELIMINARY;

PRT;

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Query Match
Best Local S
Matches 163
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EMBL; APOU2060; BAB02270.1; -.
Interpro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
PRINTS; PR00086; CYTOCHROME_P450; UNKNOWN_1.
Heme; MONOOXYGenase; Oxidoreductase.
SEQUENCE 465 AA; 53862 MW; 630A21D0765E0D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structural analysis
Sequence features of
TAC and BAC clones."
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01-OCT-2000 (TremBLrel.
01-MAR-2002 (TremBLrel.
Cytochrome P450.
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Submitted (MAY-2000)
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                                                                                                                                                                                       LFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKF
                                                                                                                                                                                                                                                                                                                                                                                                  LILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKK
                                                                                                                                                                                                                                                                                              MDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLFVISAVHLDNSRYDQPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STLQIAETLKKPEVEEYRTEFFKLVVGTLSVPIDIPGTNYRSGFQARNNIDRLLTELMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLV
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                                                        RWEENGEDKLMVFPRVSAPKGYHLKCS
                                                                                                         NWELAEDDQPFAFPFVDFPNGLPIRVS 510
                                                                                                                                                                                                                                                              MKFTRAVIFETSRLATIVNGVLRKTTHDLELNGYLIPKGWRIYVYTREINYDTSLYEDPM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSN----LSTEQILD
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32.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sato S., Nakamura Y., Asamizu E., To the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15,
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Last sequence update)
Last annotation updat
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Pred: No. 5
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                                                                                                                                                          ---YFLLFGGGVRLCPGKELGISEVSSFLHYFVTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
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A Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,

A Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,

A Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,

A Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.

A Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

A Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm G.J.,

A Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm G.J.,

A Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.

Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.

A Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

-1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

EMBL; AY050980; AAK93657.1; -.

BRIL; AY050980; AAK93657.1; -.

BRIL; AY050986; CYTOCHROME P450.

BR PIAM; PS00086; CYTOCHROME P450, UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 164
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Q949P1;
Q1-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,

Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,

Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,

Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones

Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B

Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J

Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.

Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;

Full Length CDNA of gene Af4g19230 (GI:7268718).*;

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 21, Last annotation updat)
01-UN-2002 (TrEMBLrel. 21, Last annotation updat)
Putative cytochrome P450 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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NCE 467 AA;
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LFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQ
                                                                              R------QNGSSH-----NDLLGSFMGDKEELTDEQIADNIIGV
                                                                                                            MSMDPGEEET---EQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEER
                                                                                                                                                                                                                                                                                         HAKLRKLYLRAFMPESIRN-MVPDIESIAQDSLRSW-EGTMINTYQEMKTYTFNVALLSI
                                                                                                                                                                                                                                                                                                                         HRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKHI
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                                                                                                                                                                                  -GKDEVLYREDLKRCYYILEKGYNSMPVNLPGTLFHKSMKARKELSQILARILSER
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53037 MW; 2F42
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Matches 163; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Arabidopsis cDNA clones.";
"Arabidopsis cDNA clones.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; A0505065; A4157698.1;
EMBL; AV065065; A4157698.1;
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00085; p450;
PRANTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Mguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty P1 and TAC clones.";
DNA Res. 7:31-63(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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STRAIN=COLUMBIA;
MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O9FH76 PRELIMINARY; PRT; 463 AA.

O9FH76; O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 20, Last annotation update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Cytochrome P450 (AT5945340/K9E15_12)
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Eurosids II; Brassicales; Brassicaceae; Arabidons;
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129 VGDMHRDMRSISLNFLSHARLRTTLLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLM 188
                                                              62 AAKORRYGSVEKTHVLGCPCVMISSPEAAKEVLVTKSHLEKPTEPASKERMLGKQAIFFH 121
                                                                                                                                                         69
                                                                                                                                                                                                                                              14 LLPSLLSLLLFLILLK-----RRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDEM 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                Monooxygenase; Oxidoreductase.
NCE 463 AA; 52366 MW; CCD17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      488 -AEDD----QPFAFPFVDFPNGLPIRVSR 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331 RVIQETLRVASILSFTFREAVEDVEYEGYLIPKGWKVLPLFRNIHHSADIFSNPGKFDPS 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 CVINETLRLGNYVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPW 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273
                                                                                                                     QQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVL 128
                                                                                                                                                                                    GASDGIQYGPFALP----QNGLPIVLAR 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRICAGSELAKLEMAVETHHLVLKFNWEL- 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IFAARDTTASVMSWILKYLAENPNVLEAVTEEQMAI-RKDKEEGES-LTWGDTKKMPLTS 330
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----VAPKPNTFMPFGNGTHSCPGNELAKLEMSIMIHHLTTKYSWSIV 437
                                                                                                                                                                                                                                                                                                                24.5%; Score 658; DB 10; Length 4
31.8%; Pred. No. 3.3e-39;
tive 95; Mismatches 184; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            CCD17293F553F812 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              Length 463;
                                                                                                                                                                                                                                                                                                                70;
                                                                                                                                                                                                                                                                                                             Gaps
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	Db 434 WSIVGPSDGIQYGPFALPQNGLPIALER 461	
	FVD	
HHLTTKYR 433	Db 387 FDPSRFEVAPKPNTFMPFGSGIHSCPGNBLAKLEISVLIHHLTTKYR 433	
CHHLVLKFN 484	QY 425 FNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSBLAKLEMAVFIHHLVLKFN 484	
ADIFSDPGK 386	327 PLTYRVIQETLRAATILSETEREAVEDVEYEGYLIPKGWKVLPLFRNIHH	
NSRYDOPNL 424	CY 365 DETQCVINETLRIGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNL 424	
LTWEDTKKM 326		
: / : /	Db 260 TICVITANA DOMEN STREET : : : : : : : : : : : : : : : : : :	
	Qy 305 ILSLLFAGHETSSVAIALAIFFLOACPKAVERI.PERHI ETABAKKET GEGET ATTENTION	_
LTDEQIADN 268	236 LSKRRQNPSSHTDLLGSEMEDKAGLTDEQIADN 268	_
LSTEQILDL 304		
ELAQILANI 235	OV 246 MERBET DIVIDING TO THE TOTAL OF THE HEAVER AND THE THE MANKAR	
	Db 180 LISILGKDEVYYREDIKROVYTI ECONOMYTY DOTTO :: : :	_
TILKFIERK 245	QY 189 AKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERK 245	
: : MKTYTENVA 179	Db 122 QGDYHSKLRKLVLRAFNPDAIRN-MVPHIESIAQESLNSWDGTQLNTYQ-EMKTYTFNVA 179	

Search completed: June 10, 2003, 21:58:53 Job time: 52 secs

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